

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 104996

TO: Phillip Gambel Location: cm1/9e12

Art Unit: 1644

Friday, October 03, 2003

Case Serial Number: 09758173

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Gambel,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

RUSH

09/758173



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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
OFFRAHING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: O7-JUN-1995
ATTONEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 31,030
REFERENCE/POCKET NUMBER: 012712-131
TELEFONE: 703-836-620
TELEFAX: 703-836-620
TELEFAX: 703-836-620
TELEFAX: 703-836-620
TELEFAX: 71,03-836-620
TELEFAX: 71,03-836-636
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                   US-00-488-376-17
US-08-634-223-17
US-08-634-400-17
US-08-634-400-17
US-08-70-057-17
US-09-335-6978-17
US-09-335-6978-17
US-09-744-002-17
US-09-746-002-17
US-08-26-098-11
US-08-26-098-11
US-08-26-098-11
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US-09-049-672A-21
PCT-US96-13152-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08487550 Patent No. 6113898 GENERAL INFORMATION:
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  MOLECULE TYPE: peptide
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ZIP: 22314
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LOCATION:
US-08-487-550-7
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Query Match
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  2003, 13:10:05; Search time 76.372 Seconds (without alignments) 8304.972 Million cell updates/sec
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1437
1 ATGGGTTGGAGCCTCATCTT......CCCTGTCTCCGGGTAAATGA 1437
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-476-275-2
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US-08-478-967A-3
US-08-819-866-2
US-09-343-485A-2
US-09-027-449-68
US-09-027-449-68
US-09-027-449-68
US-09-234-340A-68
US-09-121-952A-68
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US-09-234-340A-68
US-09-234-340A-68
US-09-68-375-19
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                           version 5 - 2003 C
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Maximum Match 100%
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                           GenCore (c) 1993
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seq length: 2000000000
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DB 1021 CACCAGGACTGGAAAGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCA 1080	RESULT 2 US-09-526-098-7 US-09-526-098-7 Sequence 7, Application US/09526098 Sequence 7, Application US/09526098 Setent No. 6492134 GENERAL INFORMATION: APPLICANT: Anderson, Darrell R. TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF, TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS". NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria STATE: VA COUNTRY: USA	
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	361 TACATITCACATIGEGGGGGGGGTGTTAGGTATGTTCGAATTCTGGGGCCAG 420	661 TCCAGGAGTGCTCAGGACTCTAGCAGCGAGCGTGGTGACCGCCCCCGGGCTGTCCCCCCGGCTGTCCCCCCGGCTGTCGCCCCCC

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US-09-948-429B-7
1127
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Sequence 230, Appli
Sequence 130, Appli
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Sequence 25, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 111, Appli
Sequence 511, Appli
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                                                                                                    ; Search time 284.274 Seconds
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2: (cgn2_6/ptodata/2/pubpna/PCT_KTW_PUB.seq:*
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5: (cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: (cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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Compugen Ltd.
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2 US-10-291-532-7

3 US-10-124-805-7

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US-09-822-830A-572

US-09-925-299-230

2 US-09-825-299-230

2 US-09-825-299-230

2 US-09-848-832-1

2 US-09-848-832-1

3 US-10-066-895-25

3 US-10-066-895-27

US-09-822-849A-111

0 US-09-822-830A-571

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US-09-822-830A-171
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                GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM nucleic - nucleic search, using sw model
                                                                                                      2003, 19:53:01
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length: 2000000000
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

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Anderson, Darrell R.
FENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
FENTION: TO HUAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
FENTION: PHARMACEUTHAL COMPOSITIONS CONTAINING, AND USE THEREOF
FENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                               CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380
                                                                                                                                     AAGCCGCGGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 1020
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                                         CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA
CCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10124807
Publication No. US20030166207A1
GENERAL INPORMATION:
TITLE OF INVENTION: "MONKEY MONCE
TITLE OF INVENTION: TO HUMAN B7.1
TITLE OF INVENTION: TO HUMAN B7.1
TITLE OF INVENTION: IMMUNOSUPPRESA NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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____EFF: 699 Prince Street
CITY: Alexandria
STATE: VA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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 INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 Dasse pairs
TYPE: nucleic acid
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Best Local Similarity 100.
Matches 1437; Conservative
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MOLECULE TYPE: peptide
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			П	AAW63763		AAU11644	AAW01820	ABP58275	AAR42162	AAY29458	AAB30322	AAY77766	ABU59512
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WPI; 1998-286601/25. N-PSDB; AAV35487.

ALIGNMENTS

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Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Tell/M cell interaction; tumour; inflammation; imaging agent; Vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; I cell proliferation.
                                                                                        Macaque primatized 7B6 heavy chain protein.
                     AAW63763 standard; Protein; 478 AA
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                                                                  (first entry)
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                                                                                                                                                                                                                             14-MAY-1998
                                            AAW63763;
RESULT 1
            AAW63763
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Human; macaque monkey; light chain; primatised antibody; 756 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; b7_1 antigen; CD80; b7_2 antigen; CD86; b cell cancer; metastasis; tumour; b cell lymphoma; b cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;

interleukin-2; IL-2; mutant; mutein.

Chimeric - Homo sapiens.

- Macaca sp.

Synthetic.

Chimeric

WO200189567-A1.

29-NOV-2001

Protein sequence of primatised form of the heavy chain of 7B6 antibody

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This sequence represents a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new monclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipons and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppress.
                         New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                       4b; 87pp; English.
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478 AA; Sequence Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as

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Hanna N,

Anderson DR,

WPI; 2002-089895/12. N-PSDB; AAS17245.

22-MAY-2001; 2001WO-US16364 22-MAY-2000; 2000US-0576424

(IDEC-) IDEC PHARM CORP

Example 8; Fig 4b; 89pp; English.

allergy

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DPEVKENMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHODMLNGKEYKCKVSNKALP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
                                                                                                                                                                                                          YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                                                                                                                                                                                                                                             YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180
                                                                                                                                                                                                                                                                                                                                                  KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
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                                                                                                                                                            GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                     1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                     MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                              FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                      Gaps
100.0%; Score 2561; DB 19; Length 478; 100.0%; Pred. No. 4.2e-152; Live 0; Mismatches 0; Indels 0;
                                 478; Conservative
Query Match
Best Local Similarity
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating theseses such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, systemic lupus, erythematosus, indopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or fissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative collitis, food-related allergies e.g. migraine, rhinitis and eccema, and other types of allergies. The present protein sequence represents the heavy chain of 786, a primatised antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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Best Local Similarity
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AAU11644 standard; Protein; 478

AAU11644 RESULT

(first entry)

12-MAR-2002

AAU11644;

XX

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 09:07:34; Search time 21.0061 Seconds (without alignments) 2188.349 Million cell updates/sec October Run on:

US-09-758-173-8
2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478 Perfect score: Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283308 Total number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gamma-1 chain	gamma-3 chain	gamma-3 chain	g gamma-2	chain	noclona	b	g gamma-	g gamma-	g heavy cha	gamma-	g gamma-	g gamma-2b	g gamma 2a	g gamma-	g gamma	g gamma ch	g gamma	g gamma	g gamma 3 chain	g gamma-	g heavy ch	g gamma-3 heavy	g gamma-1 c	g gamma-2b	g gamma-1	amma-3 chain	g gamma-1 chai	Ig gamma-3 chain C
SUMMARIES	ДI	Снно	A23511	A60764	GZHU	G4HU	PC4436	522080	S37483	\$31459	869339	S40295	G2MS11	S01321	147159	S31866	147160	PT0207	147158	GHRB	147161	G2GP	C30554	G3HUWI	PS0017	PS0018	GIMS	G3MSC	GIMSM	G3MSM
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an.	Query Match		ω,	m,	62.5	ä	œ		57.3	S.	ď.	55.3	4	N	σ	49.0	48.9	48.8	47.9	47.9	47.8	47.3	45.2	45.0	44.8	44.6	44.4	•	44.2	44.0
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Ig gamma-2a chain	gamma-2a	gamma-25	gamma-2c		Ig gamma-2 chain C		Ig gamma 4 chain c		heavy		Ig Y heavy chain (Ig gamma-1 heavy c	Ig mu chain precur	Ig heavy chain (DO	The state of the s
G2MSA	G2MSAB	G2MSAM	S00847	PS0019	S06611	G2MSBM	147162	538864	S04845	S69340	B46529	A49444	S14683	S69131	
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ALIGNMENTS

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RESULT 1
GHHU

Ig gamma-1 chain C region - human
C; Species: Home saptens (man)
C; Date: 31-Jan-1981
C; Date: 31-Jan-1981 # sequence.
C; Date: 33-Jan-1981 # sequence.
C; Date: 31-Jan-1982
C; Date: 31-Jan-1981 # sequence.
C; Date: 31-Jan-1982
Nucleic Acids Res. 10, 4071-4079, 1982
A; Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A; Reference number: A93433 # MUD: 82274238; PMID: 6287432 `
A; Residues: 1-330 * FELL
A; Residues: EMBL: 217370
A; Cross-references: EMBL: 217370
A; Note: Lys-330 is removed after translation
B; Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A; Reference number: 833904
A; Accession: S38614
A; Accession: S38614
A; Accession: S38614

A;Molecule type: DNA A;Ross-references: EMBL:217370 A;Cross-references: EMBL:217370 Cell 29, 671-679, 1982 A;Title Structure of human immunoglobulin gamma genes: implications for evolution of A;Reference number: \$33887; MUID:83001943; PMID:6811139 A;Accession: \$33887

A; Molecule type: DNA A; Residues: 88-113;235-330 <TAK> A; Cross-references: BMBL: 217370 B; Cruntingham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma B; Cohemistry 9, 3161-3170, 1970 A; Title: The covalent structure of a human gammaG-Immunoglobulin. VII. Amino acid seq A; Rottence number: A90563; MUID:71064024; PMID:5489771 A; Contents: myeloma protein Eu A; Accession: B90563

A; Molecule type: protein
A; Residues: 1-96, Xr, 98-135 <CUN>
A; Residues: 1-96, Xr, 98-135 <CUN>
A; Residues: 1-96, Xr, 98-135 <CUN>
A; Note: this sequence has the Glm(3) marker, 97-Arg
B; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A; Reference number: A90564; MUID:71064025; PMID:5530842

A; Contents: Eu A; ApoS64 A; Molecule type: protein Ni A; Molecule type: This sequence has the Glm(non-1) markers, 239-Glu and 241-Met R; Ponsting1, H; Hilschmann, N. R; Ponsting1, H; Hilschmann, N. R; Ponsting1, H; Hilschmann, N. A; Hiller's Z. Physiol. Chem. 357, 1571-1604, 1976, A; Hiller's Z. Physiol. Chem. 357, 1571-1604, 1976, A; Hiller Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni A; Hitle: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

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conv
                    19 gamma-3 chain C region (allotype G3m(b)) - human (Spamma-3 chain C region (allotype G3m(b)) - human (Spamma-3 thomo sapiens (man) (C) spaceis: Homo sapiens (man) (C) Date: 28 Dec-1087 #septence_revision 28 Dec-1987 #text_change 23 Jul-1999 (C) Accession: A23511 (Crawford, D.H.; Lefranc, M.P.; Lefranc, G.) (Mucleic Acids Res. 14, 1779-1789, 1986 A). Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A; Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
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C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C; Keywords: immunoglobulin homology <IMM>
F; 20-85/Domain: immunoglobulin homology <IMM>
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl.,
A;Reference number: A60764; MUID:90007613; PMID:2571587
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; Pred. No. 4.1e-89;
10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.5%;
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Best Local Similarity
Matches 308; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-377 <HUC>
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A; Residues: 1-377 <HUC>
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A;Gene: GDB:IGHG3
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SEQUENCE FROM N.A.
MEDLINE-82274238; PubMed=6287432;
Ellison J.W., Berson B.U., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINB-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
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MEDILINE-71064025; PubMed=5530842;
Rulishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.
Edelman G.M.:
                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
IGHG1.
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HV21_MOUSE
HV17_MOUSE
MUC_MESAU
HV22_MOUSE
HV23_MOUSE
MUCB_HUMAN
HV25_MOUSE
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HV32_MOUSE
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Copyright (c) 1993 - 2003 Compugen Ltd.
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DISULFIDE BONDS.
MEDLINE=71064027; FubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin.

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P03988

MUC_RABIT HV26_MOUSE MUCM_RABIT MUC_SUNMU

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K -> R (IN GIM(3) MARKER).

/FIId=VAR_003886.

D -> E (IN GIM(NON-1) MARKER).

/FIId=VAR_03887.

L -> M (IN GIM(NON-1) MARKER).

/FIId=VAR_03887.
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INTERCHAIN (WITH HEAVY CHAIN)
INTERCHAIN (WITH HEAVY CHAIN)
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Best Local Similarity 99.7
Matches 329; Conservative
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                                                                                                                                                                                                                                                    Delsenhofer J.;

"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";

Blochemistry 20:2361-2370(1981).

"In MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKERS IN THE ALSO DIFFERS IN THE AMIDATION STATES OF 35,116,198,269 & 272.

"MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 15,116,198,269 & 272.

"MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 15,116,106,177,195,198, 269, AND 272 AND IN THE ORDER OF RESIDUES 268-272.
                                                                                         Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's 2. Physiol. Chem. 357:1515-1540(1976).
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GO; GO:0003823; F:antigen binding activity; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003009; IG_MHC.
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MEDLINE=81208100; PubMed=7236608;
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HINGE.
CH2.
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                                                        DISULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
 Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PIR, A93433, GHUU.
PDB, IFC1, 15-JUL-92.
PDB, ID52, 15-JUL-92.
PDB, ID58, 09-FEB-00.
PDB, ID51, 09-FEB-00.
PDB, ID51, 09-FEB-00.
PDB, ID71, 17-MAY-00.
PDB, IFCC, 20-JUL-92.
PDB, ITZ, 108-MAY-01.
PDB, IIX; 16-MAY-01.
PDB, IIX; 16-MAY-01.
PDB, IIX; 16-MAY-01.
PDB, IIX; 16-MAY-01.
PDB, IL6X; 10-APR-02.
PDB, ICX; 10-APR-03.
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Mo-structure.
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MIM; 147100;
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68 SSMSS--SSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSY 125
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                               08vea0 mus r

06ga6 homo s

0921k1 mus r

0921k1 mus r

091k2 mus r

091z07 mus r

091z07 mus r

091z07 mus r

091z01 homo s

08bur0 homo s

08bur0 homo s

08bur1 mus r

09bur1 mus r

09bur1 mus r

09bur1 mus r

09k17 mus r

09k17 mus r

09k17 mus r

09k24 homo s

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Q8vcv5 mus n
Q8vcx4 mus n
Q99la6 mus n
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.2%; Pred. No. 1.4e-180;
Matches 416; Conservative 15; Mismatches 27; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC024289, AAHJ2189.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_W.
Ffam; PF00047; Ig, 4.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00835; IG_LIKE; 4.
Hypothetical protein.
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471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Last annotation update)
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08WUKI
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096GA6
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0921KI
091WP5
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091WP1
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091WP1
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Q96EY0
Q8WUX4
Q96AA6
Q8K0F2
Q91WR1
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Q8VCX4
Q99LA6
Q91WT3
Q91X92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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TISSUE-Spleen;
 SEQUENCE
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Q8n4y9 homo sapien
Q8tc63 homo sapien
Q8r3v9 mus musculu
Q8nf17 homo sapien
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                                                                                                         2, 2003, 08:56:23; Search time 46.2581 Seconds (without alignments) 2666.544 Million cell updates/sec
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                                                                                                                                                                       US-09-758-173-8
2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Q8N4Y9
Q8TC63
Q8R3V9
Q8R3V9
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096R3H6
096R3H6
096R3H6
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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sp_phage:*
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Match Length
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Perfect score:
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TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK 245
   FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNT 236
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                                                                                                                                                                                   254 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                         RGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
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Wataryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC025985; AAH25985.1; -.
InterPro; IPR000923; BlueCu_1.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003506; Ig_MKC.
InterPro; IPR003596; Ig_V.
Fam: PF00047; Ig; 4.
SMART; SMO0406; IGV; 1.
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s; Pred. No. 5.1e-151;
33; Mismatches 67;
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Matches 357; Conserv
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01-JUN-2002 (
01-MAR-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 181
                                       PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 241
                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                 235 VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 294
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                                                                                                                                                                                175 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178; AAH33178.1; -
InterPro: IPR00710; Ig-like.
InterPro: IPR003597; Ig_c1.
InterPro: IPR003597; Ig_LAHC.
InterPro: IPR003596; Ig_W.
InterPro: IPR003596; Ig_W.
SMART; SM00407; IgG.1; 3.
SMART; SM00406; IgW; 1.
PROSITE; PS00239; Ig_LKE; 4.
PROSITE; PS00239; Ig_LMHC; 2.
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Last annotation update)
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TISSUE-Primary B-Cells from Tonsils;
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521 AA; 57156 MW;
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Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Hyporhetical protein, Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-487-550-8
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Sequence 16,
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    /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
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US-09-526-098-8

US-09-026-985-71

US-09-026-985-71

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US-09-026-985-71

US-09-679-397-2

US-09-679-397-2

US-09-679-397-2

US-09-679-397-2

US-09-109-7-101A-7

US-09-101A-7

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Maximum Match 100%
Listing first 45 summaries
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Sequence 8, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "O HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACHUIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

ITLE OF INVENTION: PHARMACHUIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: 699 Prince Street
CITY: Alexandria
CONTRY: USA
CONTRY: USA
ZIP: 22314
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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                                                   US-08-793-450-8
US-09-740-002-25
US-09-80-49
US-09-526-098-4
US-09-740-002-27
US-09-301-593-49
US-09-741-744-81
US-08-704-744-81
US-08-704-7741-81
US-09-485-737B-67
US-09-485-737B-67
US-09-485-737B-90-05-09-12
US-09-485-737B-90-05-09-12
US-09-487-737B-90-05-09-12
US-09-487-737B-90-05-09-12
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                                                                                                               Gaps
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APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SOURNESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                          .
0
                                                                  Length 478;
                                                                                                             Indels
                                                                Score 2561; DB 4;
Pred. No. 1.2e-198;
; Mismatches 0;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCHWARE: Winbatin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION ATA:
RAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/09027449 Patent No. 6025158
                                                                                                               ;
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                                                                Query Match
Best Local Similarity 100.0%;
Matches 478; Conservative 0
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    protein
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APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               240
GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVXYCTTS 120
                                          GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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                                                                                       YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                             PPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CIIY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKID, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECHONUS. 703-836-620
TELECHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09526098 Patent No. 6492134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 478 amino acids
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MEDIUM TYPE: Floppy
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TOPOLOGY: linear
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CLASSIFICATION:
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1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-124-58-71

US-10-225-108A-3

US-10-225-108A-3

US-10-227-694-5

US-10-227-694-5

US-10-227-694-5

US-10-227-694-5

US-10-227-694-5

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US-10-386-974-2
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Maximum Match 100%
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ALIGNMENTS

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
                                                                                                                                                                                         STREET: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Bexandria STATE: VA COUNTRY: USA 21P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFENCE/DOCKET NUMBER: 012712-131
FELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/487,550
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
Sequence 8, Application US/09948429B Patent No. US20020177689A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
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Sequence

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Indels
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
                                                   US 08/487,550
                APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/10291532; Publication No. US20030180290A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 703-836-6620
                                 FILING DATE:
APPLICATION NUMBER: US 08
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                           TELEFAX: 703-836-2021
INPORMATION FOR SEG ID NO:
SEGUENCE CHARACTERISTICS:
LENGTH: 478 amino acids:
                                                                                                                                                                                                                                                                                                                                                                  al Similarity 100.
478; Conservative
                                                                                                                                                                                       703-836-2021
                                                                                                                                                                                                                                                                                         ) MOLECULE TYPE: protein US-10-124-807-8
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US-10-291-532-8
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                         Length 478;
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                                                                                                                                                    100.0%; Score 2561; DB 10;
100.0%; Pred. No. 1.2e-169;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10124807
Publication No. US20030166207A1
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              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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703-836-2021
                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                  amino acid
GY: linear
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STATE: VA
                                                                                                                                                                        Best Local Similarity
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CLASSIFICATION:
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 TELEFAX:
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APPLICAMY: HANNA, NABIL
APPLICAMY: HANNA, NABIL
TITLE OF INVENTION: ANTI-CDE0 ANTIEDDY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TILLE REPERENCE: 037003/291872
CURRENT APPLICATION NUMBER: 05/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR APPLICATION NUMBER: 09/758,173
                                                                                                                                                                                                                                    GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
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                                                                                                                   1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
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Length 478;
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October 2, 2003, 13:01:50; Search time 1867.6 Seconds (without alignments) 15574.362 Million cell updates/sec
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711
ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 711
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	600 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	69 Home 03 Home 03 Home 71 Home 71 Home 16 Home 122 Home Human Human 16 Seq. 06 Seq. 07 Home 60 Seq. 08 Seq. 07 Home	linear PAT 14-FEB-2001 stowsky,W.S. and Heard,C.
DB	1 6 AR108866 1 6 AR265200 1 6 AR265200 5 9 AR064208 6 BD176841 0 9 BC020233 7 9 AR064143 9 AR064149 5 9 AR064149 6 9 AR064140 7 9 AR064140 7 9 AR064141 7 9 AR064120 8 9 AR064206 9 HSIGVLO02 1 9 AR064220 4 9 AR064220 6 9 AR064220 7 9 HSIGVLO02 8 9 AR064220 9 HSIGVLO02 9 HSIGVLO02 9 HSIGVLO02 9 HSIGVLO02 9 HSIGVLO02 9 AR064226 9 AR064226 9 AR064226 9 AR064226	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ALIGNMENTS 711 bp DNA 2825142 2825142 11) 12) 12) 13, Hanna, N., Shefalf, primatized antibodies antibodies 38-A 9 05-SEP-2000;
* Query Match Leng		2	AR108866 Sequence 9 from AR108866 AR108866.1 GI:1 Unknown. Unclassified. 1 (bases 1 to 7 Anderson,O.R., B Human B7.1-specil expressing said Patent: US 61138
. ت			RESULT 1 AR108866 LOCUS DETNUTION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

FEATURES Location/Qualifiers source 1.711 Acganism="unknown" BASE COUNT 160 a 226 c 193 g 132 t	Query Match Best Local Similarity 100.0%; Score 711; DB 6; Length 711; Best Local Similarity 100.0%; Pred. No. 5.8e-174; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 1 ATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTCTGCT	OY 61 GAGTCTGTCCTGACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120	QY 121 TCGTGCACTGGGACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 180	QY 181 CCAGGAACGCCCCCAAACTCCTCATCTATGACATAACAAGCGACCTCAGGAATTTCT 240 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300 [11]	OY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 360	AN 361 TTCGGAGGAGCCGGCTGACCGTCCTAGGTCACCCAAGGCTGCCCCTCGGTCACT 420	OY 421 CIGITCCGCCTCCTGAGGAGTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480	QY 481 AGTGACTTCTACCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAG 540	OY 541 GCGGGAGTGGAGACCACCACCACCACAAAGAAAGAAGAAGAAGTACGCGGCCAGCAGC 600	OY 601 TACCTGAGCCTGAGCATGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660	OY 661 CATGAAGGACACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711 1111111111111111111111111111111111	111 bp DNA linear PAT 27-AUG-2 inding interactions between certain 37.1 and B7.2 co-stimulatory antigens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 711) AUTHORS Anderson,D.R., Hanna,N., Brams,P. and Hard,C.
FEATURES Location/Qualifiers source 1.711 //Organism="unknown" base count 160 a 226 c 193 g 132 t	Query Match. 100.0%; Score 711; DB 6; Length 711; Best Local Similarity 100.0%; Pred. No. 5.8e-174; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 ATGAGGGTCCCCGGTCAGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT 60	Qy. 61 GAGTCTGTCCTGACACCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120	QY 121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCTC 180	Qy 181 CCAGGAACGGCCCCAAACTCCTCATCTATGACATTAACAAGGGACCCTCAGGAATTTCT 240	QY 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGCCTCCCTGGCCATCACTGGGCTCCAG 300	QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCTGAATGCTCAGGTA 360 	QY 361 TTCGGAGGACCCGGCTGACCGTCCTAGGCCAAGGCTGCCCCCTCGGTCACT 420	QY 421 CTGTTCCGCCCTCTGAGGAGCTTCAAGCCAACAAGCCAACTGGTGTGTCTCATA 480	QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGGATAGCAGCCCCGTCAAG 540	QY 541 GCGGGAGTGGAGACCACCACCTCCAAAGCAAAGCAACAAGTACGGGCCAGCAGC 600	QY 601 TACCTGAGGCCTGAGGAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG 660	Oy 661 CATGAAGGAACACGTGGAAGACACAGTGGCCCTACAGAATGTTCATGA 711 1111111111111111111111111111111111	T 2 200 200 ITION SION SION SION E E	REFERENCE 1 (bases 1 to 711) AUTHORS Aguin,S. and Vezina,LouisP. TITLE Method for producing polyhydroxyalkanoates in recombinant organisms JOURNAL Patent: US 6492134-A 9 10-DEC-2002;

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Title: Perfect :

Sequence:

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Run on:

Scoring table:

Minimum DB Maximum DB

Database

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Human benign prost Lung cancer relate Human immune Syste Human igd anti-rhe Human igd anti-rhe Human igd anti-rhe Human rype antihum Plasmid scPv(CC046 Human type antihum Human polymucleoti DNA encoding novel Human polymucleoti DNA encoding novel DNA encoding novel Human immune syste Human immune syste Human prostate exp Human secreted profuman secrete
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Human lung specifi
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Gene #3746 used to
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/product= 16C10 light chain
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                  AAX06954
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AAT62509
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    AAV35488 standard; DNA; 711
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  Macaque primatized
DNA sequence of a
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Primatised anti-hu
                                                                                                                             2, 2003, 12:12:30; Search time 145.625 Seconds (without alignments) 13179.730 Million cell updates/sec
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N_Ceneseq_19unus;

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT:*

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT:*

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT:*

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT:*

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1985.DAT:*

SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1985.DAT:*

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SIDS1/gcgdata/geneseq/geneseqn.emb1/NA2001.DAT:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAT62512
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                                                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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97WO-US19906 96US-0746361

29-OCT-1997; 08-NOV-1996;

Human immune syste Human cancer statu Sequence encoding Plasmid Glambda-1B Plasmid Glambda-1B

AAL50812 AAQ03609 AAC84209 AAC84207

709.4 582.6 573 571.4 565.2 558.8

10m450ra

Score

Result Š. 14-MAY-1998

099

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Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; PT_1 antigen; CD86; PC_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of a primatised form of the light chain of 16C10 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CDB6) and/or B7.2 antigen (CDB6) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leuksemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoia arthritis, psoriasis, aplastic anaemia, inflammatory bile diseases, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression
                                                                          AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAG
                                                                                                                                       TACCTGAGCCTGAGGCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
                                                GCGGGAGTGGAGCCACCACCACCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such \epsilon
                                                                                                                                                                                                                            661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
                                                                                                                                                                                                                                                         /*tag= a /*tag= a /*tag= /*tag= antibody" /product= "Light chain of 16C10 antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Chimeric - Macaca sp.
Synthetic.
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                                                                                                                                                                                                                                                                                                                This sequence encodes a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving a cell/B cell interactions, particularly autoimmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. on set diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunosopens to develop anti-idlotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleaving (11-2), T cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
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                                                                                                                                                             New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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antigen-specific immunoglobulin G (IgG) responses.
                                                                                                                                                                                                                                                                            Example 7; Fig 5a; 87pp; English.
                                                     Hanna N;
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       PHARM CORP
                                                  Brams P,
                                                                                         WPI; 1998-286601/25.
                                                                                                                      P-PSDB; AAW63764
       (IDEC-) IDEC
                                                     Anderson DR,
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AGENCOURT

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mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6278335
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602724089
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                  BX462166
                                                                                                                                                                                                                                                                         BX449367
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisosience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2466 row: c column: 08
High quality sequence start: 10
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BM918688
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BG757977
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BG758242
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AGENCOURT_8353826 NIH_MGC_113 Homo
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BX449367
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BQ711292
BQ711292.1 GI:21850191
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Homo sapiens
521.8
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BQ711292
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BQ708635 AGENCOURT
BQ708570 AGENCOURT
BG685644 602637629
                                                    2003, 13:05:20 ; Search time 1175.83 Seconds (without alignments) 14696.420 Million cell updates/sec
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1 ATGAGGGTCCCCGCTCAGCT.......CCCCTACAGAATGTTCATGA 711
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                                                                                                                                                            45562784
       5.1.6
Compugen Ltd.
                                                                                                                                                         Total number of hits satisfying chosen parameters:
        GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                       OM nucleic - nucleic search, using sw model
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Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

on:

Run

Sequence:

Scoring table:

569.2 562.6 559 558.6

Score

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/clone_lib="NIH_MGC_113"
/clone_logan: Spleen; Vector: porB7; Site_1: XhoI; Site_2:
DcoR1; cDNA made by oliqued Triming. Directionally cloned
GGCAGGG(G). Library constructed by Linq Bnog in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
10 c 230 g 167 t lothers
                                           BQ708635 913 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312
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NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MG clone distribution information can bfound through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLCM2476 row: i column: 01
High quality sequence stop: 663.
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Pred. No. 1.9e-128;
0; Mismatches 75;
                                                                                                                                                                                                                                                                                           Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/clone="IMAGE:6282312"
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BQ708635
BQ708635.1 GI:21847534
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al Similarity 88.9%;
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                                                 /organism="Homo sapiens"
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//dol_type="mRNA"
//dol_type="mRNA"
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ECORI; oDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Homy in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Pred. No. 4.5e-130;
0; Mismatches 78;
ity sequence stop: 655.
Location/Qualifiers
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Local Similarity 88.6%;
Nes 629; Conservative
High quality
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us-09-758-173-9.rni

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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
US-09-592-998C-7
US-09-702-705-433
US-09-702-705-1625
US-09-736-457-1625
US-09-736-457-1625
US-08-991-89A-241
US-09-598-326-241
US-09-598-326-241
US-09-620-312D-62
US-09-702-705-409
US-09-736-457-409
US-09-736-457-409
US-08-305-683A-3
US-08-305-683A-3
US-08-305-683A-3
US-08-305-683A-3
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US-09-070-817-4
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                                                                                                                                                                                                                                                                                    ALIGNMENTS
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Patent No. 6113898
GENERL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFRENCE/POCKET NUMBER: 0127:
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-836-6620
TELEFRAX: 703-836-2221
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SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: "MODITIES OF INVENTION: TO ITILE OF INVENTION: PAR. TITLE OF INVENTION: IMM NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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US-08-487-550-9
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1 ATGAGGGTCCCCGCTCAGCT.......CCCCTACAGAATGTTCATGA 711
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... /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
... /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
... /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
... /cgn2_6/ptodata/2/ina/BECOMB.seq:*
... /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
... /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
... /cgn2_6/ptodata/2/ina/Packfiles1.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-526-098-9
US-08-487-5524-20
US-08-26-098-1
US-09-526-098-1
US-09-045-098-1
US-09-045-098-1
US-09-152-060-47
US-09-152-060-29
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US-09-736-457-1589
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                                                                                           2003, 13:10:05 ;
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                                                                - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEYAGENT INFORMATION:
NAME: TESKID, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECHONE: 703-836-6620
TELEFAX: 703-836-2021
            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                   US/09/526,09
                                                                                                     09/383,916
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                                                                                                                                                                                                                                                                        : 711 base pairs
nucleic acid
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Matches 711, Conservative
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                                       DATA
                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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            OPERATING SYSTEM:
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LOCATION:
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US-09-526-098-9
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Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN BY.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF PITTLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SECUENCES: 12
CORRESPONDENCE ADDRESS:
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                       Mismatches
100.08; ±14.001
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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        Best Local Similarity 100. Matches 711; Conservative
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180 240 300 360 360 420 540 540 120 61 GAGTCTGTCCTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGGTCACCATC 120 240 300 CIGITCCCGCCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATA 480 9 1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGTGGCTCCCAGGTGCACGATGT 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGCTCCAG 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAATGCTCAGGTA 481 AGIGACTICTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGAIAGCAGCCCCGTCAAG 61 GAGICIGICCIGACACAGCCGCCCTCAGICTCIGGGGCCCCCAGGGCAGAAGGICACCAIC 121 TCGTGCACTGGGAGCACCTCCAACATTGGAGGTTATGATCTACATTGGTACCAGCAGCTC 181 CCAGGAACGCCCCCAAACTCCTCTATGACATTAACAAGCGACCCTCAGGAATTTCT 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 361 TTCGGAGGAGGACCCGGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT 1 ATGAGGGTCCCCGCTCAGCCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT .; Length 711; 100.0%; Score 711; DB 4; I 100.0%; Pred. No. 2.6e-186; ive 0; Mismatches 0; Version #1.30

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2, 2003, 19:53:01; Search time 140.653 Seconds (without alignments) 12894.584 Million cell updates/sec
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1 ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 711
version 5.1.6
- 2003 Compugen Ltd.
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Maximum Match 100%
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Copyright (c) 1993
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                       Perfect
                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Published_Applications_NA:*

Database :

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/cgn2_6/ptodata//2/pubpna/US60_NEW_PUB_seq:*

13206, A 4, Appli 5, Appli 4, Appli 5, Appli 70, Appli Appli Appli Appli Appli 799, Sequence Sequence Sequence 5 Sequence 1 Sequence 4 Sequence 5 Sequence Seq Description Sequence Sequence US-10-198-846-13206 US-09-747-669-4 US-10-290-73-4 US-10-290-703-4 US-10-158-646-70 US-10-198-846-12799 US-10-158-646-71 US-09-948-429B-1 US-10-124-807-1 US-10-291-532-1 US-10-291-532-9 US-10-124-905-9 US-10-073-138-5 US-09-948-429B-9 SUMMARIES Query Match Length DB Score 5551.8 5552.6 5552.6 5552.6 5552.6 5552.6 550.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 50.0 5 Result õ

Sequence 1, Appli	Sequence 1, Appli	4 1	37	71		- '	Sequence 3, Appli		٠.	٠.	•		-	47	4	20	Sequence 29, Appl	CA	~	σ	1327	Н	128	ທ	101	87,	Sequence 89, Appl
	-10-0/3-138-1	-09-954-456-7		-09-873-319-7	-09-960-106-1	-198-846-1	-194-80	5-10-198-84	S-10	-10-198-846	-10-158-64		353-161-47	US-09-852-659A-47	US-09-852-797-47	US-09-853-161-29	US-09-852-659A-29	US-09-852-797-29	US-10-158-646-76	US-09-972-656-95	US-10-198-846-13276	US-10-225-108A-13	US-10-198-846-12838	US-10-211-357-5	US-09-972-656-101	US-09-972-656-87	US-09-972-656-89
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705	2112	915	915	915	915	2635	705	2635	1640	1597	883	1597	882	882	885	879	879	879	2667	642	1565	726	895	702	654	651	648
76.0	7.0	74.9	74.9	74.9	74.9	74.8	74.2	73.9	71.8	71.3	70.9	9.69	68.1	68.1	68.1	67.9	67.9	67.9	66.7	66.5	66.3	66.3	66.2	62.9	65.7	65.6	65.2
540.2	2.040	532.2	532.2	532.2	532.2	531,8	527.6	525.4	510.6	507	504.2	494.6	484.2	484.2	484.2	482.6	482.6	482.6	474	473	471.6	471.2	470.4	468.4	466.8	466.2	463.4
17	0 0	20	21	22	23	24	25	56	27		59					34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Anderson, Darrell R.

WENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

VENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
APPLICATION NUMBER: 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6-6-20
                      Sequence 9, Application US/09948429B Patent No. US20020177689A1
                                                                                                                                                                                                                                                              ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street
                                                               GENERAL INFORMATION:
APPLICANT: Anderson, Dar
TITLE OF INVENTION: TO BE
TITLE OF INVENTION: PHAR
TITLE OF INVENTION: PHAR
TITLE OF INVENTION: IMMC
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                            Alexandria
                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   22314
US-09-948-429B-9
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US-10-124-807-9
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                                                                                                                                                                 Score 711; DB 10;
Pred. No. 5.4e-206;
; Mismatches 0;
                                                                                                                                                               Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 711; Conservative 0;
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRRACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                     ) NAME/KEY: mat_peptide
; LOCATION: 1..711
US-09-948-429B-9
                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                               1...711
                                                                                      NAME/KEY:
LOCATION:
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Sequence 9, Application US/10124807 Publication No. US20030166207A1 GENERAL INFORMATION:

RESULT 2 US-10-124-807-9

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Darrell R.
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMEOSITIONS CONTAINING, AND USE THEREOF AS
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                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 711; DB 12;
ilarity 100.0%; Pred. No. 5.4e-206;
Conservative 0; Mismatches 0;
                                                                                         NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORING DATE: NO-JUN-1995
NAME: Teskin, Robin L.
                                                                           IMMUNOSUPPRESANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           012712-131
                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 711 base pairs
nucleic acid
EDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
APPLICANT: Anderson,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
1..711
                                                                                                                                                                     Alexandria
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Best Local Similarity
Matches 711; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                   STREET:
CITY: Al
STATE: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

sed sed

Minimum DB Maximum DB

Database

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Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/Bb cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaque primatized 16C10 light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                             ABG80711
ABR01477
ABG19293
AAG64472
                                                                                                                                                                                                                                                 ABR01467
ABR01473
ABR01463
ABR01468
ABR01488
AABR01488
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ABR01476
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ABR01479
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  97WO-US19906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-286601/25.
N-PSDB; AAV35488.
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Anderson DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998
RESULT 1
Primatised anti-hu
Human immune syste
Moncolonal antibod
Novel human diagno
Human lung specifi
Human anti-TIMP-1
Human anti-TIMP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaque primatized
                                                                                2, 2003, 08:56:23 ; Search time 27.6933 Seconds
(without alignments)
1352.654 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqype-mbl/AAA1981.DAT:*
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| SIDSI/gcgdata/geneseqp-embl/AAA1981.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AAA1984.DAT:*
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| SIDSI/gcgdata/geneseqp-embl/AAA1990.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA2002.DAT:*
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1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 236
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AAW01821
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1232 1232 1229 1052.5 1006 1001 999.5 992.5

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Result

Human type antihum
Plasmid scFV(CC046
Antibody D light c
Human anti-TIMP-1

Human type antihum Human type antihum Human anti-TIMP-1

Human immune syste Human immune syste Amyloid peptide co Human anti-TIMP-1 Novel human diagno

Antibody HB4C5 lig Monoclonal rabies Novel human diagno

Anti-HIV-1 recombi Human IgG anti-rhe Primatised anti-hu Macaque primatized Protein sequence o

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This sequence represents a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28 Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sclerosis, graft vs. Inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases. B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CDS interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRVPAQLLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1232; DB 19; Length 236; 100.0%; Pred. No. 1.2e-66; tive 0; Mismatches 0; Indels 0;
                                                                                                           5a; 87pp; English.
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CDB0) and/or B7.2 antigen (CDB0) for inducing the apoptosis of B7+ cells. The invention is useful for inducing the apoptosis of B7+ cells. The invention is cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leakaemia, and autoimmune diseases such as Gellspip concert, lymphoma, B cellspip concert, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple solerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating resistance to or rejection of transplanted dorgan or tissue for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 16010, a primatised antibody used in the invention to induce apoptosis and inhibit production of

Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as

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Brams

WPI; 2002-089895/12 N-PSDB; AAS17246

Anderson DR,

(IDEC-) IDEC PHARM CORP

22-MAY-2001; 2001WO-US16364 22-MAY-2000; 2000US-0576424

29-NOV-2001.

Example 8; Fig 5a; 89pp; English.

allergy

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PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1232; DB 23; Length 236; 100.0%; Pred. No. 1.2e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graft-vs-host disease; immunosuppression; organ rejection;
interleukin-2; IL-2; mutant; mutein.
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Primatised anti-human B7.1 antigen antibody 16C10 light chain.

Chimeric - Homo sapiens. Chimeric - Macaca sp. - Macaca sp

WO200189567-A1

Synthetic.

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interleukin-2 (IL-2).

lambda chain lambda chain lambda chain Vlambda chain prlambda chain prlight chain prelight chain pre-

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Ig lambda chain precursor - human c) Species: Homo sapiens (man) C) Species: Journ-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C; Accession: S05270; S04601

R; Kishimoto, T. So5270
A; Accession: S05270
A; Coss.references: EMBL:X14583; NID:933394; PIDN:CAA32725.1; PID:933395
A; Cross.references: EMBL:X14583; NID:99296497; PMID:2500644
A; Reference number: S04601; MUID:99296497; PMID:2500644
A; Accession: S04601
A; Molecule type: mRNA
A; Reference number: S04601; MUID:99296497; PMID:2500644
A; Accession: S04601
A; Molecule type: mRNA
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1 ambda chain - human
C; Species: Homo sapiens (man)
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Ig lambda chain V region - human
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C; Species: Homo sapiens (man)
C; Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C; Accession: 82928
R; Chouchane, L.; Van Spronsen, A.; Breyer, J.; Guglielmi, P.; Strosberg, A.D.
Bur. J. Blochen. 207, 1115-1121, 1992
A; Reference number: 829257; MUID:92362614; PMID:1499555
A; Reference number: 829257; MUID:92362614; PMID:1499555
A; Reterence number: 829257; MUID:92362614; PMID:1499555
A; Reterence number: 829257; MUID:92362614; PMID:1499555
A; Redering prediminary
A; Molecule type: mRNA
A; Residues: 1-216 <CHO>
A; Note: only part of the coding sequence is given
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Seywords: pyrroglutamic acid
F; 131-199/Pomain: immunoglobulin homology <INM>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S25757
R;Combriato, G; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-234 <COM>
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1.8e-58;
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Pred. No. 1.6e-58;
9; Mismatches 11;
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20; Mismatches
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Best Local Similarity 83.0%;
Matches 191; Conservative 2
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Accession: 825752
R;Combriato, G; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamphacession: 825752
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
R;Combriato, G; Klobeck, H.G.
R;Combriato, G; Klobeck, H.G.
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immuno
A;Reference number: S16439; MUID:91257162; PMID:1904362.
A;Reference number: S16439; PMID:1904362.
A;Reference n
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Pred. No. 5.4e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=1150336; PubMed-5549568;
MEDILINE=1150336; PubMed-5549568;
Ponstingl H., Hess M., Hilschmann N.;
Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Rern). V. The complete amino acid sequence and its genetic interpretation.";
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MEDLINE-95255298; PubMed-7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
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MEDLINE-74109253; PubMed-4814727;
Chen B.L., Poljak R.J.;
"Amhor acid sequence the (lambda) light chain of a human myeloma immunoglobulin (IgG New).";
Biochemistry 13:1295-1302(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
P06318 P04431 P04431 P01714 P01714 P01714 P01602 P01602 P01608 P01608 P01719 P01719 P01715 P0
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
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                KVIW_HUMAN

IV3A_HUMAN

IV3E_HUMAN

IV6E_HUMAN

KVIJ_HUMAN

KVIJ_HUMAN

IV7E_HUMAN

IV7E_HUMAN

IV7E_HUMAN

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Biochem. J. 110:631-652(1968).
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Copyright (c) 1993 - 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 294:536-540(1981).

-I MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS H, X, AND NIG-64. THE KERN PROTEIN HAS THE KERN PROTEIN HAS THE MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER.

-I MISCELLANGOUS: SIX TANDEM LAMBDA TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDAMED-6273747; MEDIAMED T.A., Leder P.; Maldmann T.A., Leder P.; Meterer P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.; "Clustered arrangement of immunoglobulin lambda constant region genes
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90133913; PubMed-2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWN.
MEDLINE-75046825; Pubmed-4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                               Saul F.;
"The three-dimensional structure of the fab' fragment of a human myeloma immunoglobulin at 2.0-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panagiotopoulos N.;
"Rotational allomerism and divergent evolution of domains in immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
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                                                                                                                                                                                MEDLINE-75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
"Primary structure of the Mog lambda chain.";
Biochemistry 13:4102-4114(1974).
                                                                                                                                                                   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00253; AAA59107.1; -.
EMBL; L38562; AAB36581.1; ALT_INIT.
EMBL; X51754; CAB38569.1; ALT_INIT.
EMBL; X51755; CAA36049.1; -.
EMBL; X51755; CAA36051.1; -.
                           3ur. J. Biochem. 228:886-893(1995).
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HGNC:5856; IGLC2
HGNC:5857; IGLC3
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2MCG; 15-JUL-92.
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1AQK; 04-FEB-98.
1LIL; 15-MAY-97.
               immunoglobulins.";
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Genew; HGNC:
Genew; HGNC:
MIM; 147220;
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Nature 29
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InterPro; IPR007110; ig-like.
InterPro; IPR003597; ig_c1.
InterPro; IPR003065; ig_MHC.
Pram; Pr00047; ig; 1.
SMART; SW00407; iGc1; 1.
PROSITE; PSS0835; iG_LIKE; 1.
PROSITE; PS00290; iG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Bence-Jones protein;
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01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Immunoglobulin lambda-like polypeptide l precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (CD179b antigen)
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"Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
expressed in pre-B cells and may encode the human immunoglobulin
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-89315835; PubMed-2501791;
Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
                                                                                                                                                                                                                    INTERCHAIN (WITH HEAVY CHAIN).
A -> N (IN MCG+ MARKER).
FIIG=VAR_003898.
S -> T (IN WGC+ MARKER).
S -> G (IN KERN+ MARKER).
FIIG=VAR_003890.
T -> K (IN MCG+ MARKER).
T -> K (IN MCG+ MARKER).
T -> K (IN MCG+ MARKER).
R -> K (IN 02+ MARKER).
FIIG=VAR_003901.
R -> K (IN 02+ MARKER).
FIIG=VAR_003902.
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100.0%; Pred. No. 1.2e-36;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 105; Conservative
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Q8KOF8 mus musculu Q8KOF8 mus musculu Q9fala5 mus musculu Q9fal0 homo sapien Q9fjd homo sapien Q9fg homo sapien Q9fg qinglymosto Q9182 homo sapien Q9052 qinglymosto Q9052 qinglymosto Q90536 mus musculu Q8KIf0 mus musculu M8KIf0 musculu M8KIf0 musculu Q8KIf0 musculu M8KIf0 m
Q91w12 mus musculu QBr062 mus musculu QBvc16 mus musculu Q99w21 was musculu Q91w89 mus musculu Q81w68 mus musculu Q8rc58 mus musculu Q8rc98 mus musculu Q8r028 mus musculu
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Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymochetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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TISSUB-TONSI;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020233; AAH20233.1;
InterPro; IPR003065; Ig_MHC.
InterPro; IPR0030596; Ig_V.
Ffam; PS00247; ig; 2.
SMART; SM00406; IGv; 1.
RPSOITE; PS00290; IG_MHC; 1.
RPSOITE; PS00290; IG_MHC; 1.
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84.8%; Score 1045; DB 4; Length 2
Best Local Similarity 88.4%; Pred. No. 2.2e-83;
Matches 205; Conservative 10; Mismatches 15; Indels
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Q99W37
Q91WS9
Q91WF8
Q9TE63
Q8VC55
Q8R028
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Q96SB0
Q96SB0
Q96JC1
Q96JD2
Q96JD1
Q96JD1
Q9NSD6
Q9NSD6
Q9UC824
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Q8tcd0 homo 9
Q8nek0 homo 9
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Q8wtu6 ]
Q96e61 ]
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Q8n355
Q8tbc9
Q8n5f4
Q96i69
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Q8nekl
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: SP_archea:*
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3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_ammal:*
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sp_unclassified:*
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sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                  80.5%; Score 991.5; DB 4; Length 236; 83.1%; Pred. No. 1e-78; Live 12; Mismatches 26; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 977.5; DB 4; Length 236; 81.8%; Pred. No. 1.7e-77; ive 20; Mismatches 21; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 TKPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
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Strausberg R.;
Strausberg R.;
Submitted JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC030944; AAH30984.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-11ke.
InterPro; IPR003597; Ig.-c1.
InterPro; IPR003597; Ig.-c1.
InterPro; IPR003596; Ig_-MHC.
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012876; AAH12876.1; -.
Interpro; IPR00110; Ig-11ke.
InterPro; IPR003006; Ig-MrC.
InterPro; IPR003066; Ig-WrC.
PFam; PF00047; Ig; 2.
PFAMT; SM00406; IGV; 1.
PROSITE; PS00290; IG-NHC; 1.
                                                                                                                                                                 .l protein.
236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25024 MW; 1703B77942630E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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SMART; SM00409; 1G; 2.
SMART; SM00407; 1Gcl; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 101-MAR-2003 (TrEMBLrel. 23, 14) Hypothetical Protein.
                                                                                                                                                                                                                                                      Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189; Conservative
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SEQUENCE 236 AA; 2
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                 Hypothetical SEQUENCE 23
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Matches
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QBNEJ1
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 TRLIVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                    TITPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVIHEGSTVEKTVAPIECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVIHEGSIVEKTVAPIECS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 84.8%; Score 1045; DB 4; Length 237; Best Local Similarity 88.4%; Pred. No. 2.2e-83; Matches 205; Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022099; AAH22098.1; -
InterPro; IPR007110; Ig-11ke.
InterPro; IPR03306; Ig_MHC.
InterPro; IPR03596; Ig_W.
SMART; SMO0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Tonsil;
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Strausberg R.;

Q96E61 RESULT 3 Q96E61

HAPPEN SERVICE SERVICE

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2, 2003, 09:12:09; Search time 10.4815 Seconds (without alignments) 952.662 Million cell updates/sec
                                                                                                                                                                                  US-09-758-173-10
1232
1 MRVPAQLIGLLILMLPGARC.......COVTHEGSTVEKTVAPTECS 236
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                              using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                          OM protein - protein search,
                                                                                                                October
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                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                             Sednence:
                                                                                                              Run on:
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seq length: 0 seq length: 20000000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

328717 segs, 42310858 residues

Searched:

328717

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/AA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* იო4ro. რ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

App] Sequence 9, Sequence 9, Patent No. 51 Sequence 14, Sequence 10, Sequence 10, Description Sequence 7 Sequence 4 Sequence 2 Sequence Sequence Sequence Sequence Sequence Sequence Sequence (Sequence Sequence Sequence Seguence Sequence Sequence US-08 487-550-10 US-09-526-098-10 US-09-372-425A-7 US-08-487-550-2 US-08-487-550-2 US-08-672A-1 US-09-049-672A-1 US-09-152-060-8 US-09-152-060-8 US-09-152-060-8 US-09-152-060-8 US-08-153-050-10 US-08-153-101-9 US-08-733-450-6 US-08-733-450-6 US-08-733-450-6 US-08-733-450-6 US-08-733-450-6 US-08-733-450-6 US-08-731-74-21 US-08-721-101-9 US-08-422-091-9 US-09-313-942-14 US-09-025-769B-170 US-07-916-098A-56 JS-08-422-112-9 SUMMARIES 5189147-10 Length Query Match 1 100.0 885 882 857.5 836 804.5 634.5 634.5 567 567 548 544.5 543 543 525 Score Result Š.

Sequence 5, Appli	Sequence 153, App	15	_	Sequence 16, Appl	Н	Sequence 26, Appl	4, A	Sequence 6, Appli	Sequence 4, Appli	Sequence 11, Appl	24,	Sequence 20, Appl	Sequence 2, Appli	Sequence 18, Appl	m	Sequence 6, Appli
US-08-157-101A-5	US-08-899-575-153	US-08-899-575-153	PCT-US95-08743-153	US-08-812-586-16	US-09-535-832A-17	US-09-740-002-26	US-08-305-683A-4	US-09-049-672A-6	PCT-US94-07659-4	US-09-079-029-11	US-09-740-002-24	US-09-479-614-20	US-07-690-192-2	US-09-025-769B-18	US-08-353-400-37	US-08-487-550-6
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236	235	235	235	235	235	234	131	234	234	310	234	242	234	112	239	239
41.3	41.2	41.2	41.2	40.8	40.8	40.5	40.3	40.0	40.0	40.0	39.3	39.2	39.5	38.6	38.6	38.3
508.5	508	508	508	.502.5	502.5	499	496.5	492.5	492.5	492.5	484.5	483	482.5	476	475	472
28	30	31	32	e B	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
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                                                                                                                                                                                                                                                                                                              COMPUTER: USA

CIP: 2214

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: TESKIN, Robin L.
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1232; DB 3; Best Local Similarity 100.0%; Pred. No. 1.7e-91; Matches 236; Conservative 0; Mismatches 0;
                                      Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                            E: BURNS, DOANE, 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703-836-2021
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MOLECULE TYPE: protein

US-08-487-550-10
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CITY: Alexandria
STATE: VA
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RESULT 1
US-08-487-550-10
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Sequence 3

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66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.4%; Score 1052.5; DB 3;
88.3%; Pred. No. 4.2e-77;
tive 10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
CLASSIFICATION: 536
PRIOR APPLICATION: 536
APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Incyte Pharmaceuticals, Inc. 3174 Forter Drive Palo Alto
                                                                                                                                                                                       Sequence 7, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PR
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                Au-Young, Janice
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cerrone, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                              Lal, Preeti
Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 204; Conservative
                                                                                                                                                                                                                                                                              Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: ADRETUTOS
CLONE: 2492122
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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APPLICANT:
APPLICANT:
                                                                                                                                                                   US-09-049-672A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Pa
STATE: C.
COUNTRY:
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHRNACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
FGGGTRLIVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                          1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OFFICE OFFICE ALL COMPACTION CONTROL OF STATEM STATEM SCHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/526,098 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1232; DB 4; 100.0%; Pred. No. 1.7e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                               RESULT 2
US-09-526-098-10
; Sequence 10, Application US/09526098
; Patent No. 64921...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Alexandria
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 236 amino acids
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Best Local Similarity 100.
Matches 236; Conservative
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CLASSIFICATION:
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                                                                                                                                                          2, 2003, 09:18:44; Search time 88.5965 Seconds (without alignments) 421.442 Million cell updates/sec
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1 MRVPAQLIGLILIMLPGARC.......CQVTHEGSTVEKTVAPTECS 236
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// Ggn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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// Ggn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/PCTUG2_BUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// Ggn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-121-807-10
US-10-121-807-10
US-10-124-905-10
US-09-747-669-6
US-10-124-905-10
US-10-194-801C-4
US-10-194-801C-4
US-10-194-807-2
US-10-124-905-2
US-10-124-905-2
US-10-124-905-2
US-10-124-905-2
US-10-124-905-1
US-09-974-4449-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587654 seqs, 158212981 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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        Sequence 102, Appl 18

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        US-09-972-656-102
        Sequence 102, Appl 19

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        US-09-972-656-102
        Sequence 96, Appl 20

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        Sequence 108, Appl 20

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        US-09-972-656-108
        Sequence 70, Appl 20

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        Sequence 70, Appl 20

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        US-09-852-654-108
        Sequence 70, Appl 20

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        US-09-852-109-10
        Sequence 81, Appl 20

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        US-09-852-109-10
        Sequence 82, Appl 20

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        US-09-852-109-10
        Sequence 12, Appl 20

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40 635.5 51.6 9.246 9.201-299A-90 Sequence 10, Appl 455.5 51.6 9.246 9.201-299A-10

41 635.5 51.6 9.246 9.201-299A-10

42 569.5 46.6 139 10.910 0.9-291-299A-10

567 46.6 139 10.910 0.9-929-664-51

567 45.6 139 10.910 0.9-929-664-50

ALIGNMENTS

ALIGNMENTON: DAWNEY MONGCLOAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS NUMBER OF SEQUENCES:

ADDRESSES: ADDRESSES:

ADDRESS
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9

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Sequence 10, Application US/10291532

Fublication No. US20030180290A1

GENERAL INFORMATION:
APPLICANT: HARHARAN, KANDASAWY
APPLICANT: HARHARAN, KANDASAWY
APPLICANT: HARNA, NABIL
TITLE OF INVENTION: ANTI-CD80 ANTIEODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
CURRENT APPLICATION NUMBER: 02/310,291,532
CURRENT APPLICATION NUMBER: 09/758,173
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2091-01-12
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1995-06-07
NUMBER: OF SEQ. ID NOS: 12
NUMBER: OF SEQ. ID NOS: 12
                                                                                                                                                                                                                                                                    61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                         FGGGTRLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRVPAQLIGILILIMIPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
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                                                                                                                                                                                1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                            AGVETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGVETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: primatized peptide sequence (Synthetic 105-10-291-532-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                          Length 236;
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6.6e-90;
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100.0%; Score 1232; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e-90;
Matches 236; Conservative 0; Mismatches 0;
                                                                                        100.0%; Score 1232;
100.0%; Pred. No. 6.6
iive 0; Mismatches
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                                                                                                             Best Local Similarity 100.
Matches 236; Conservative
                         TYPE: protein
                           ; MOLECULE TYP
US-10-124-807-10
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US-10-124-607-10
US-10-124-607-10

Sequence 10, Application US/10124807

Publication No. US20030166207A1

GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: "MONEEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEGITAL.COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                         1 MRVPAQLLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                            Query Match 100.0%; Score 1232; DB 10; Length 236; Best Local Similarity 100.0%; Pred. No. 6.6e-90; Matches 236; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: CALCALLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 012712-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,030
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TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: TESKID, RODIN L.
REGISTRATION NUMBER: 35,0
                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 236 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 amino acids
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703-836-2021
                                                                                               TOPOLOGY: linear; MOLECULE TYPE: protein US-09-948-429B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22314
  TELEFAX:
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COUNTRY:
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Title: Perfect score: Sequence:	US-09-758-173-11 1431 1 ATGAACACCTGTGGTTCTT	CCCTGTCTCCGGGTAAATGA 1431	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0		
Searched:	2888711 seqs, 20454813386 residues	iues	
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Description	AR108867 Sequence BD065139 Identific AR108863 Sequence BD065135 Gequence BD065135 Gequence BD065135 Gequence BD065135 Gequence BD065135 Gequence BD065135 Gequence AR05775 Homo sapi AK087775 Homo sapi AK087775 Homo sapi AK087775 Homo sapi AK15537 Sequence AR15537 Sequence AR05282 Sequence AR05282 Sequence AR05282 Sequence AR05282 Sequence AR05284 Sequence AR30061 Process f BC000501 Process f BC01477 Homo sapi AK08789 Homo sapi AR331186 Sequence AR331185 Sequence AR331185 Sequence AR331185 Plasmid DNA A22585 H. Sequence AX33125 Flasmid DNA A22585 H. Sequence AX17257 Homo sapi	linear PAT 14-FEB-2001 owsky, W.S. and Heard, C.
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EATURE SO ASE CO	S Location/Qualifiers urce 1. 1431		QY Db	961 CGGGAGGAGCAGTACAACAGCACGTACGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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Oy Db	1 ATGAAGACTOTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60 1		QY	
0 v	GIGCAGCIGCAGGAGTCGGGCCCAGGACTGGIGAAGCCIICGGAGACCCIGICCCICACC 1		QY Db	1141 CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGGTCAAAGGC 1200
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QY	301 CTGAAGCTGAACTCTATGACCGCGGGGGCGGGGGTGTTACTGTGTGAGAGATCGT 360 		Qy Db	1381 CTGCACACTACACGAGAAGAGCCTTGCCTGCTGCGGGTAANGA 1431
da da	361 CTTTTTCAGTIGTIGGAATGGTTTACAACAGGTTCGATGTCTGGGGCCCGGGAGTC 420 		RESULT 2 AR265201 LOCUS	AR265201
Qy Db	421 CIGGICACCGICICCTCAGCTAGCACCAAGGGCCCATCGGTTCCCCCTGGCACCCTCC 480 		ACCESSION VERSION KEYWORDS	AR265201 GI:29693622
Qy Db	481 TCCAAGAGCACCTCTGGGGGAAGAGGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC 540		SCURCE ORGANI REFERENC	Σ
QY	541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 600		AUTHORS TITLE JOURNAL FEATURES	<pre>S Aquin, >. and Vezina, Louis, F. Method for producing polyhydroxyalkanoates in recombinant organisms IL Patent: US 6492134-A 11 10-DEC-2002;</pre>
QY	601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660		SOUTC BASE COUNT ORIGIN	υ
Qy Db	661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720 		Query Match Best Local. Matches 143	Match 100.0%; Score 1431; DB 6; Length 1431; Local Similarity 100.0%; Pred. No. 6.2e-277; es 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy Db	721 GACAAGAAAGGGGCCCAAATCTTGTGACAAAACTCACAGGCCCAGGGCCCAGGA 780 		Qy Db	1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
Qy	781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCTC 840 		QY	61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAACCTTCGGAGACCCTGTCCCTCACC 120
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Qy Dp	901 GAGGICAAGTICAACIGGIACGIGGACGCGIGGAGGIGCATAAIGCCAAGACAAAGCCG 960 		QY Db	181 CCAGGAAGGGCTGGAGTGGATTGGGAGTTTCTATAGTAGTGGGAACACCTACTAC 240

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October 2, 2003, 12:12:30 ; Search time 293.094 Seconds (without alignments) 13179.730 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Primatised anti-hu Macaque primatized DNA sequence of a Primatised anti-hu Macaque primatized DNA sequence of a Human immune syste Monoclonal antibod
SUMMARIES	AAY62513 AAV35489 AAS17247 AAV35485 AAV35485 AAV35485 AAV366522 AAV18059
DB	1 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
% Query Match Length DB ID	1431 1431 14431 14431 14431 1431 1567 1431
% Query Match	100.0 1000.0 1000.0 1000.0 1000.0 8899.2
Score	1431 1431 1431 1315.8 1315.8 1315.8 1276.4
Result	10845078

Human immune syste Anti-rhesus D reco Human gamma-4 heav Human gamma-4 pep	Human gamma-4E hea Nucleotide sequenc Hepatitis C virus Human anti-RSV mon CDNA of the heavy Human monoclonal r	immun colon anti- benig adeno cancer cancer	Traget plasmid Man Bncodes heavy chai Plasmid Glambda-1B Monoclonal antibod Monoclonal antibod Plasmid Glambda-1A Macaque primatized DNA sequence of a Plasmid Hulghdrood	Place Pride
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ALIGNMENTS

AAT62513 standard; DNA; 1431 BP.

RESULT 1

AAT62513;

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Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
                                                                                         Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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Chimeric Homo sapiens.
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Shestowsky WS;

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Brams P,

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                                                                                                             CCTGAACTCCTGGGGGGACCGTCACTCCTCTTCCCCCCAAAAACCCCAAGGACACCCTC
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                                                                                            CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
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                                                                                                                                  2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAM01821 and AAW01822) of the light and heavy chain of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody forms (Cloned 16C10 1914) and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow produ. of primatised antibody in e.g. CHO cells. Primatised 7010 and 736 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
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October 2, 2003, 13:05:20 ; Search time 2366.54 Seconds (without alignments) 14696.420 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery Score Match Length DB ID Descrit C 1 944 66.0 1201 13 BX377695 BX377 C 2 929.6 65.0 1142 13 BX414495 BX414 BQ062 C 4 899.2 63.0 1020 12 BQ062878 BQ062 C 4 899.2 62.8 1045 13 BX337477 BX337477			Description .	BX377695 BX377695	BX414495 BX414495	BO062878 AGENCOURT	BX337477 BX337477
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg-CS0CAP001AE07NP1scluster=7198.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0CAP001AE07NP1.
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/clone_libe"Homo sapiens THYMUS"
/clone=libe"Homo sapiens THYMUS"
/clone=vector: pCMVSPORT_6 ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into Library was not normalized."
/ 27 others
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization
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98.2%; Pred. No. 1.1e-211;
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/mol_type="mxRA"
/db_xref="taxon:9606"
/clone="CS0CAP001Y113"
/tissue_type="THYMUS"
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                                                                                               /clone="CSDIO9YJ10"
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/clone_lib="Homo sapiens PlacENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PlacENTA COT 25-NORMALIZED"
/note="lst strand cDNA was prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V dises of the pCMVSPORT 6 vector. Library was normalized."
296 c 396 g 267 t 54 others
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Faraday Avenue Genoscope sequence ID : CSODI009DE05NP1.
Location/Qualifiers
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Pred. No. 4e-215;
'; Mismatches 22;
                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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95.8%;
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B'.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACECTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, A
Sequence 68,
Sequence 68,
     Sequence 3, Sequence 7, Sequence 7, Sequence 6, Sequence 3, Sequence 3, Sequence 3, Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68
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Sequence 2
Sequence 3
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                    US-09-343-485A-3

US-08-487-550-7

US-08-187-101A-7

US-08-187-101A-7

US-08-187-101A-3

PCT-US95-09576-3

US-08-187-0957-3

US-08-147-0957-3

US-08-476-915A-3

US-08-476-915A-3

US-08-476-915A-3

US-08-419-86-2

US-09-343-485A-2

US-09-343-485A-2

US-09-027-449-68

US-09-121-952A-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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MOLECULE TYPE: peptide
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STRANDEDNESS:
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ZIP: 22314
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  2, 2003, 13:10:05 ; Search time 76.0531 Seconds (without alignments) 8304.972 Million cell updates/sec
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Sequence 11, Appl
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                                                                                                                                                                                                                                                      Sequence 17
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Seguence 7
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Db 1021 GACTGGCTGAATGGCAAGGTACAAGTGCCAAGCACCTCCAACACCCCC 1080	RESULT 2 US-09-526-098-11 Sequence 11, Application US/09526098 Fatent No. 6492134 GENERAL INFORMATION: FATEL INFORMATION: FOR INVENTION: FOR	COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC CONDATIBLE CORPORTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/526,098 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: 09/383,916 FILING DATE: APPLICATION NUMBER: 09/383,916 FILING DATE: 00 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION: NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 012712-131 FILEPHONE: 703-836-6620 TELEPHONE: 703-836-6620 TELEPHONE: 703-836-6620 TELEPHONE: AND ASSESSION OF TELEPHONE: TRIBERANT TONEY TO
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 0; Gaps 0; Indels 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 1431; Gaps Gap	361 CTTTTTCAGTTGTAGAATGGTTTACAACTGGTTCGGGGCCCGGGAGTC 420 1	69 661 AGCTTGGGCACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720 60 AGCTTGGGCACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAGTG 720 61 AGCTTGGCAACCTACATCTGCAACGTGAATCACAAGCCCAGCAAGGTG 720 62 ACAAGAAACACAGACCCAAATCTTGTGAACAAACTCACAACCCCACCACACACCCCCACACAACCCCACCA

Sequence 1, Appli Sequence 230, App Sequence 230, App Sequence 19, Appl Sequence 789, App Sequence 1604, App Sequence 445, App Sequence 745, App

Sequence 101, Apple Sequence 15, Appl Sequence 1, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 20, Appli Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli

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    GenCore
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Sequence 27, A.
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Sequence 571, A.
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Sequence 11, Application US/09948429B

Sequence 11, Application US/09948429B

Sequence 11, Application US/09948429B

Patent No. USZO020177689A1

GENERAL INFORMATION: MONOELONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: MUNOSUPPRESANTS"

CORRESPONDENCES 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC Compatible
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COMPUTER: Patentin Pc-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/948,429B
FLING DATE:
APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN 1995
ATTORNEY/AGENT INPORMATION:
NAME: TESKIA, ROBIN L.
RAME: TESKIA, ROBIN L.
REPERBERATION UNMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 1,

US-10-225-108A-1

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INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1431 base pairs TYPE: nucleic acid STRANDEDNES: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE: NAME/KEY: CDS CATION: 1.1431 FEATURE: NAME/KEY: mat_peptide LOCATION: 1.1431 LOCATION: 1.1431	Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGAAACACCTGTGGTTCTTCCTCCTGTGGGAGCTCCCAGATGGGTCCTGTCCCAG 60	8=8 8=8	OY 181 CCAGGGAAGGGCTGGAGTGGAATTCTATAGTAGTAGGAACACCTACTAC 240	E-E	QY 361 CTTTTTTCAGTTGTAGATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420 Db 361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420 QY 421 CTGGTCACCGTCTCCTCAGCTAGCACCATCGGTCTTCCCCCTGGCACCTCC 480 Db 421 CTGGTCACCGTCACCTAGCTAGCACCAACGGTCTTCCCCCTGGCACCTCC 480	ပ္-ပ္ ဗ္-ဗ္	ပ္ျပ္ ဖ-စ	4-4 U-

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Primatised anti-human B7.1 antigen antibody 16C10 heavy chain. AAW01822 standard; Protein; 476 AA. (first entry) 25-MAY-1997 AAW01822; AAW01822

Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rhemmatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma Chimeric Macaca cynomolgus; Chimeric Homo sapiens. WO9640878-A1. 19-DEC-1996.

96WO-US10053. 95US-0487550. (IDEC-) IDEC PHARM CORP. 07-JUN-1995; 06-JUN-1996;

Brams P, Hanna N, Shestowsky WS;

Anderson DR,

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                                                                                   2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human b7.1 antigen monoclonal antibody 16610. Cloned 16610 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7010 and 786 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
                                                                                                                                                                                                                                                                                                     1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                             100.0%; Score 2549; DB 18; Length 476; 100.0%; Pred. No. 5.8e-149; Ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaque primatized 16C10 heavy chain protein.
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                                                                  81pp; English.
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                                                                                                                                                                                                                                                                  476; Conservative
 1997-108638/10
                                                                  Claim 14; Fig 10B;
                                                                                                                                                                                                                                                         Similarity
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WPI; 1997-108030,
N-PSDB; AAT62513
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This sequence represents a primatized form of the antibody 16010 heavy chain from macaque. This sequence is used in a method which studies new monotonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibite binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, I filamentory bowel disease, allergy and multiple solenois, graft vs. Inflammatory bowel disease, allergy and multiple solenois, graft vs. host diseases, be cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuperessants. Blocking B7/CD28 interactions funduces long-term, antigen-specific immunosuperession, i.e. it inhibits production of interlenkin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IGG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monoclonal antibodies specific for B7.1 or B7.2 antigens and mihibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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tive 0; Mismatches 0;
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cell proliferation
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2549
1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
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SwissProt_41:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	7 bomo gan	type omod			Cavin	homo	rattu	rattus	snu snu	gnw	Snu	P03987 mus musculu	P01863 mus musculu	Snm	P01865 mus musculu	ratt	rattus	_		homod		_	homo	homo	oryct		1 ory	œ	P01873 mus musculu	24 homo	P01874 canis famil	7 meson	0 homo sa
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P18532 mus musculu	HV61_MOUSE	7	116	14.2	361	4 2	
P01825 homo sapien	HV2G_HUMAN	~	117	14.2	362	44	
P23086 heterodontu	HVC3_HETFR	-	393	14.4	366.5	43	
P18531 mus musculu	HV60_MOUSE	-	116	14.4	368	47	
P01877 homo sapien	ALC2_HUMAN	-	340	14.9	379	41	
P20758 gorilla gor	ALC1_GORGO	.—;	353	14.9	380.5	40	
P01876 homo sapien	ALC1_HUMAN	Н	353	15.0	383.5	on M	
P23084 heterodontu	HVC1_HETFR	-1	370	15.1	384	38	
P23088 heterodontu	HVCM_HETFR	Н	461	15.1	385	37	
P23087 heterodontu	HVCS_HETFR	Н	438	15.5	394	36	
P23085 heterodontu	HVC2_HETFR	Н	438	15.5	395.5	32	
P01822 mus musculu	HV46_MOUSE	Н	137	15.6	396.5	34	

ALIGNMENTS

RESULT 1	Ę)	P01857; 21-JUL-1986 (Rel.	21-JUL-1986 (Rel. 01, Last sequence up	Ig gamma-1 chain	IGHG1.		buvaryota, metazoa, thordata; tranzata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae;	NCBI_TaxID=9606;			A Ellison J.W., Berson B.J., Hood L.E.;		Nucleic Acids Res. 10:4071-4079(1982).		MEDLINE=71064024;		Waxdal M.J., Edelman G.M.,	"The covalent structure of a	acia sequence of meavy chain cyanogen bromide fragments HI-H4. Biochemistry 9:3161-3170(1970).			MEDLINE=/1064025; PubMed=5530842;		"The covalent structure of a human gamma G-immunoglobulin. 8.	acid sequence of heavy-chain cyanogen bromide fragments H5	Blochemistry				"The rule of antibody structure. The primary structure of a					SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.		"Three-dimensional structure determination of antibodies	structure of crystallized monoclonal immunoglobulin IgG1	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).		MEDLINE=710	Gall W.E., Edelman G.M.;	covarent structure
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                                                                                                                                                                                                                                          "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.8 - A resolution.";
Biochemistry 20:2361-2370(1981).
-!- MISCELLANEOUS: NIE HAS THE 61M(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS IN THE AMIDATION STATES OF 35.116,198,269 & 272.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 268-272.
                                                                               Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198, 2674272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; 3D-structure.
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003623; F:antigen binding activity; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0037110; Ig-1ike.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SWART; SMO407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
Deisenhofer J.;
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HINGE.
CH2.
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PIR; A93433; GHHU.
                                               DIŚULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PDB; ID4V; 04-0CT-00
PDB; ID4K; 06-JUN-01
PDB; IHZK; 06-JUN-02
PDB; IHZK; 12-JUN-02
PDB; ITZ; 16-MQC-01
PDB; ITZ; 16-MQC-01
PDB; ITX; 16-MAX-01
PDB; ILX; 16-MAX-01
PDB; ILX; 16-MAY-01
PDB; 2RCS; 12-NOV-97; GENEW; HGNC:5525; IGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1FC2; 15-JUL-92.
1AJ7; 12-NOV-97.
1D5B; 09-FEB-00.
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PDB; 1AJ7;
PDB; 1D5B;
PDB; 1D5I;
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	FF	DISULFID	144	204 308		
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•	FT		239	239	/FTIG=VAR_003886, D -> E (IN G1M(NON-1) MARKER)	
	H H H				FTIG-VAR_003887.	
	FF		241	241	L -> M (IN G1M(NON-1) MARKER). /FTIG=VAR_003888.	
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	H		260	265		
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	- (- 2, [2,		302	303 303		
	FT		305	312		
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	FJ		316	317		
	SO	SEQUENCE	n 60		1; 3770EE106C2FA33D CRC64;	
	ош.	Query Match Best Local S			Score 1763; DB 1; Length 330; Pred, No. 6.5e-114;	
	4	deciles 52	a) conser	44 L 1 V &	sdp5 (O	
	δy	147	ASTKGPSVI	PLAPSSKST	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	C)
	d G	1	ASTKGPSVE	PLAPSSKST	GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	9
	δy	207		TVPSSSLGT)TY ICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGG	7
	qq	61		TVPSSSLGT	GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	7
	QY	267	PSVFLFPPR	RENTIMISE	PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	m
	qq	121	PSVFLFPPR	PKDTLMISR	PSVELEPPRKRDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTRPREEQYN	7
	QΫ	327	STYRVVSVI	TVLHODWLN	KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	3
	qq	181	STYRVVSVI	TVLHQDWLN	STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLFPSRDE	4
	δλ	387	LTKNOVSLI	CLVKGFYPS	LTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKLTVDKSRW	44
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Q96ga6 homo s
Q8my24 homo s
Q91wp5 mus m
Q91wr1 mus m
Q91x7 mus m
Q91z07 mus m
Q91z07 mus m
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Q86dk0 homo g
Q8vcv5 mus r
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                   Q91xel mus
Q8k172 mus
                    096aa6 h
096ka8 h
096bb9 h
096bb9 h
099m21 h
099m22 m
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Q96k68 hc
Q91x92 n
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QBvea0 n
QBk0z4 n
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85.2%; Pred. No. 9.9e-162;
ive 16; Mismatches 45; Indels 9;
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Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1;
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
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SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Q95K68
Q91K68
Q96GA6
Q96GA6
Q96GA6
Q91W5X4
Q91W724
Q91W72
Q91W71
Q99KV0
Q90W71
                               Q96KX8
Q96BB9
Q8WUK1
Q99M22
Q8VCX7
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
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Q8tc63 homo sapien
Q8td79 homo sapien
Q8fd17 homo sapien
Q951c4 mus musculu
Q961d4 mus musculu
Q971a4 mus musculu
Q99131 mus musculu
Q99131 mus musculu
Q99125 mus musculu
Q99126 mus musculu
Q873h6 mus musculu
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Q95m34 equus cabal
Q96ey0 homo sapien
Q9bul0 homo sapien
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1 MKHLWFFILLLVAAPRWVLSQ.......MHEALHNHVTQKSLSLSPGK 476
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Copyright (c) 1993 - 2003
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Maximum Match 100%
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Q8R3H6
Q91ZO5
Q95FQ8
Q95FQ8
Q95FY0
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Gapop 10.0 , Gapext 0.5
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Q8NF17
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240 VDKRVESK---YGPPCPSCPAPEFLGGPSVFLFPPKFKDTLMISKTPEVTCVVVDVSQED
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178; AAH33178.1; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
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Last sequence update)
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TISSUE=Primary B-Cells from Tonsils;
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SWART; SM00407; 19:1; 3.
SWART; SM00406; 10:1; 3.
PROSITE; PS50835; 1G_LIKE; 4
PROSITE; PS00290; 1G_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222,
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01-007-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
Hypothetical protein.
Homo sapiens (Human).
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521 AA; 5
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SEQUENCE 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418
                                                                                                                          243
                                                                                                                                                                                                                                                        239 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 298
                                                                                                                                                                                                                                                                                                                               363
                                                                                                                                                                                                                            303
                                                                                                                                                                                                                                                                                                                                                                                                                              TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 PPGKGLEWIGTI-NFSGNMYXSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCAAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                   VGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                                                                                                            FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK
                                                                                                                                                      179 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK
                                                                                                                                                                                                                       244 AEPKSCDKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                                                                             299 FNWYVDGVEVENERTKPREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 PPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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Catarrhini; Hominidae; Homo.
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Strausberg R.;
Interpro; IPR000923; BlueCu_1.
Interpro; IPR003051; BlueCu_1.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003066; Ig_W.
Pfam; PF00047; ig, 4.
SMART; SM00406; IGV: Interpro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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83.2%; Pred. No. 1.7e-159;
1ve 29; Mismatches 39;
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Best Local Similarity 83.28
Matches 397; Conservative
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Homo sapiens (Human).
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SEQUENCE 4
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October 2, 2003, 09:12:09; Search time 21.1407 Seconds (without alignments) 952.662 Million cell updates/sec
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328717 Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB ID Description	118-08-487-1850-10-10-11-11-11-11-11-11-11-11-11-11-11	ישר סט ייטר סט ייטר מבילתבוונה דלי	-860-979-60-80	US-09-049-672A-4 Sequence 4, A	-08-487~550-4 Sequence 4,	US-09-526-098-4	US-08-793-450-8 Sequence 8,	US-08-397-411-7 Sequence 7,	US-08-523-894-12 Sequence 12,	US-08-523-894-8 Sequence 8,	US-08-523-894-10 Sequence 10,	US-08-887-352B-18 Sequence 18,	3 US-09-109-207C-18 Sequence 18, Appl	US-09-282-505-2 Sequence 2,	US-09-054-255-2 Sequence 2,	US-09-296-005-18 Sequence 18,	US-09-282-846-2 Sequence 2	US-09-680-145-2 Sequence 2,	US-08-887-352B-14 Sequence 14,	US-08-887-352B-16 Sequence 16,	US-08-466-151-65 Sequence 65,	US-09-109-207C-14 Seguence 14,	US-09-109-207C-16 Sequence 16,	US-09-296-005-14 Sequence 14,	US-09-296-005-16 Sequence 16,	US-09-740-002-25 Seguence 25,	US-09-740-002-27 Seguence 27	/
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Sequence 8, Appli	Sequence 7, Appli	Sequence 71, Appl	Sequence 71, Appl	Sequence 71, Appl	Sequence 71, Appl	Sequence 10, Appl	7	Sequence 2, Appli	7	7	Sequence 8, Appli	Sequence 8, Appli	13,	Sequence 8, Appli	22,	22,	Sequence 22, Appl
US-08-466-163B-8	US-09-289-942A-7	US-09-027-449-71	US-09-026-985-71	US-09-121-952A-71	US-09-234-340A-71	US-08-378-939-10	US-09-679-397-2	US-09-680-148-2	US-09-304-465A-2	US-08-157-101A-7	US-08-487-550-8	US-09-526-098-8	US-08-458-516-13	US-09-049-672A-8	US-07-934-373C-22	US-08-437-642B-22	US-08-146-206C-22
153 4	462 4	452 3	152 3	152 4	152 4	176 2	149 4	149 4	149 4	159 1	478 3	178 4	149 1	167 3	154 2	154 3	154 4
82.1	81.3	81.3	81.3	81.3	81.3	6.08	9.08	80.6	80.6	9.08	80.5	80.5	79.8	79.4	79.1	79.1	79.1
2093	2072.	2071.	2071.5	2071.5	2071.5	2063	2053.5	2053.5	2053.5	2053.5	2053	2053	2033	2024.5	2016.5	2016.5	2016.5
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ALIGNMENTS

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Sequence 12, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACETTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NDARA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TEEKTON NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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100.0%; Score 2549; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.5e-198;
Matches 476; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 476 amino acids
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                                                                                                                                      1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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                                                                                                                    1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                     Gaps
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                                                   Length 476;
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                                                   Query Match 100.0%; Score 2549; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-198; Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION UNBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
   protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-526-098-12
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APPLICANT:
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                                                                                     DKKAEPKSCDKIHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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Patent No. 6492134

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONNEX MONCCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THERBOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THER
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
PGKGLEWIGSFYSSGNTYYNPSLKSQVTISTDISKNQFSLKLNSMTAADTAVYYCVRDR
                   LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                 EPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGIQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                      KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE STORM SYSTEM: PC-DOS/MS-DOS COFWARE: PATENTIN Release #1.0, Version #1.30 APPLICATION DATA: US/09/526,098 FLLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: BIRNS. DOANE, SWECKER & MATHIS STREET: 699 Prince Street STREET: 7A lexandria STREET: 7A CONTENT OF THE STREET OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/487,550
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APPLICATION NUMBER: 09/383,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-09-526-098-12
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TOPOLOGY:
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October 2, 2003, 09:18:44; Search time 178.695 Seconds (without alignments) 421.442 Million cell updates/sec
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2549
1 MKHIWFFLLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: 587654

587654 seqs, 158212981 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Published_Applications_AA:*

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| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 12 appl	15	15	2 5	1 4			Sequence 4 April	Sequence 17 April	Segmence 8 Appl	Sequence 37 Appli	Sequence 10 Appr	Sequence 16, Appl	Seguence 18 Appl	Sequence 18, Appl
ID	US-09-948-429B-12	US-10-124-807-12	US-10-291-532-12	US-10-124-905-12	US-09-948-429B-4	US-10-124-807-4	US-10-291-532-4								US-10-113-996-18
DB	101	12	12	14	10	12	12	14	15	15	12	r.		6	12
Query Match Length DB ID	476	476	476	476	476	476	476	476	467	467	580	467	451	451	451
Query Match	100.0	100.0	100.0	100.0	90.6	90.6	90.6	90.6	84.2	84.1	83.9	83.9	83.4	83.4	83.4
Score	2549	2549	2549	2549	2309	2309	2309	2309	2145.5	2144.5	2138	2137.5	2127	2126	2126
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-292-869	US-09-920-171	-920-1	US-09-925-1	0 - 113 - 996 - 1	US-10-113-99	9 US-09-796-848A-43	S-0	US-09-996-288-2	US-09-996-56	0S-09	40	3-09-925-1	9 US-09-796-848A-49	3-09-996-288-2		96-848A-3	-796-848A-4	08-60-SD	-996-288-2	60-SD	US-09-996-265-2	3A-3		I US-09-996-265-2	-79	US-09-996-28	10 US-09-996-288-252	10 US-09-996-288-254
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ALIGNMENTS

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Sequence 12, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "HORNAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,"
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/487,550
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APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWE: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
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US-09-948-429B-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPVIVSWNSGALISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HANNA, NABIL
TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: ANTI-CD80 ANTIBODY B CELL LYMPHOMA CELLS ALONE OR
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TITLE REPREBAGE: 037003,291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRICH APPLICATION NUMBER: 60/31,187
PRICH APPLICATION NUMBER: 60/31,187
PRICH APPLICATION NUMBER: 09/758,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2549; DB 12;
100.0%; Pred. No. 1.1e-172;
iive 0; Mismatches 0;
                                                                                                                                                                    012712-131
                                          FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-001-1995
ATTORNEY/AGENI INFORMATION:
NAME: Teskin, Robin i.
REGISTRATION NUMBER: 35,030
                           09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-291-532-12

Sequence 12, Application US/10291532
PUblication No. US20030180290A1
GENERAL INFORMATION:
APPLICAMT: HARIHARAN, KANDASAMY
APPLICAMT: HANNA, NABIL
                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                       LENGIH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-10-124-807-12
        PRIOR APPLICATION DATA:
                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           amino acid
GY: linear
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Best Local Similarity
Matches 476; Conserv
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Publication No. US2000166207A1
Publication No. US2000166207A1
Publication No. US2000166207A1
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOURCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOURCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOURCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                     Length 476;
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                                                                                                                                                                               100.0%; Score 2549; DB 10;
100.0%; Pred. No. 1.1e-172;
ive 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/10/124,807
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BUNNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                  Best Local Similarity 100.
Matches 476; Conservative
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                   MOLECULE TYPE: protein US-09-948-429B-12
                                                                                 TYPE: amino acid
TOPOLOGY: linear
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US-10-124-807-12
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                        Version #1.30
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Best Local Similarity 100.0%; Pred. No. 3.7e-186;
Matches 705; Conservative 0; Mismatches 0;
                                                                                                                                         APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                   US/09/526,098
        PC-DOS/MS-DOS
                                                                            CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DAIE:
                                                                                                                                                                                    NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        nucleic acid
      OPERATING SYSTEM: PC-I
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                   APPLICATION NUMBER:
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US-09-526-098-1
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Patent No. 6492134

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HURMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IRMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                           120
                                                                                                                        CGGGCCCCTAIACTGGTCAICTAIGAIGAIAGIGACCGGCCCTCAGGGAICCCIGAGCGA 240
                                                                                                                                                                   ACCTGTGGGGGAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGCG 180
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Best Local Similarity 100.0%; P
Matches 705; Conservative 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CITY: Alexandria
STATE: VA
COUNTRY: USA
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US-09-526-098-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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MOLECULE TYPE:
FEATURE:
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FEATURE:
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US-08-487-550-1
                                                                                                                                                                                                                                                                               RESULT 1
US-08-487-550-1
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291.8
2291.8
282.8
273.2
273.2
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267.2
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7, Appli
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Sequence 833, App
Sequence 62, Appl
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Sequence 970, App
Sequence 433, App
                                                                         2, 2003, 13:10:05; Search time 37.4685 Seconds (without alignments) 8304.972 Million cell updates/sec
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Sequence 908,
Sequence 970,
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1 ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 705
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Sequence 25
Sequence 23
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-702-705-1625
US-09-736-457-1625
US-09-592-998C-7
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US-09-526-098-1

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US-09-304-90-11

US-09-304-672A-25

US-09-049-672A-25

US-09-049-672A-3

US-09-152-060-47

US-09-152-060-47

US-09-152-060-46

US-09-152-060-46
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Maximum Match 100%
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Match Length D
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Maximum DB seq
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Perfect score:
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APPLICANT: Anderson, Darrell R.

TILLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TILLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TILLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TILLE OF INVENTION: PHARWACGUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
SUBCKESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551,
                                                                                                             Sequence Seq
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                               US-09-338-933-268
US-09-215-681-268
US-09-702-705-1589
US-09-736-477-409
US-09-736-477-409
US-09-736-457-409
US-09-588-281-241
US-09-589-281-241
US-09-589-109
US-08-476-349-109
US-08-476-349-109
US-08-476-349-109
US-08-476-349-109
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US-09-620-312D-551
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NAME: Teskin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-62021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAKET: 699 Prince Street CITY: Alexandria STATE: VA COUNTRY: USA 21P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAATCAGGGAACACCCCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 TGACTCAGCCACCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAACATTACCTGTGTGG 153
                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Matson
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2474 row: 1 column: 21
High quality sequence stop: 653.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COGITCICCICCICGCCTCTCTCACTG----CACAGGCTCTGTGACCTCCTAIGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCT
                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.8%; Score 555.6; DB 13; Length 931; 89.3%; Pred. No. 1.7e-125; live 0; Mismatches 69; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                      Homo sapiens (human)
                                                                                                                    (bases 1 to 931)
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     ACCESSION
VERSION
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                                                                                        /lab_host="Noil of plage-resistant)"

/lab_host="Noil of plage-resistant)"

/note="Corgan: Spleen; Vector: pOTB7; Site_1: Xhol; Site_2:

BCORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xhol sites using the following 5' adaptor:

GGCACGA(GG, Library constructed by Ling Hong in the
laboratory of Gearald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a

NIH MGC Library.

282 c. 254 g 173 t 2 others
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                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                    Score 558.8; DB 13
Pred. No. 2.8e-126;
); Mismatches 52;
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AGENCOURT_8443486 NIH_MGC_113 Homo
5', mRNA sequence.
                              /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6279618"
cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                 0,
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91.9%;
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DEFINITION

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RESULT 2 BQ709526

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Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 952)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2469 row: h column: 19
High quality sequence stop: 584.
BQ707953 AGENCOURT
BQ712246 AGENCOURT
BQ712246 AGENCOURT
BQ712246 AGENCOURT
BQ71224 AGENCOURT
BQ716256 602712568
BM324274 AGENCOURT
BQ71556256 602712568
BM324274 AGENCOURT
BQ711587 AGENCOURT
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CB555601 MMSPOO49
BG755301 6027144044
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BG3824 GG2036250
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BG7553852 603647172
BM91437 AGENCOURT
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BG776365 AGENCOURT
BG77611 GG2709539
BG77644 AGENCOURT
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BG776441 GG2709539
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AGENCOURT 8353624 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279618
5', mRNA sequence.
BQ711447.1 GI:21850346
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 BQ707953
BQ708246
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BQ710672
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BQ72625
BM974274
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Homo sapiens
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KEYWORDS
SOURCE
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BQ709526 AGENCOURT
BQ711683 AGENCOURT
BG757730 602714835
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Copyright (c) 1993 - 2003 Compugen Ltd.
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2 DNA sequences (AAT62509 and AAT62510) respectively code for primatised forms (AAW01817 and AAW01818) of the light and heavy chain of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease. monoclonal antibody binding human $\rm B7.1~or~B7.2$ antigen for treating autoimmune disease or graft-versus-host disease Claim 7; Fig 8A; 81pp; English.

Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

ô Gaps ; 0 Length 705; Indels ; DB 18; 4.3e-167; 0 / Match Local Similarity 100.0%; Pred. No. 4.3 hes 705; Conservative 0; Mismatches Query Match Best Loca Matches

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661 GGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 705

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AAV35484 standard; DNA; 705

ВР

AAV35484;

(first entry) 29-SEP-1998

chains

Macaque primatized 7C10 light chain DNA.

CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Toell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; Toell proliferation; ss. Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80;

Macaca fascicularis.

Location/Qualifiers .705

/product= 7C10 light chain Q

WO9819706-A1

9 9

14-MAY-1998

97WO-US19906 29-OCT-1997;

96US-0746361 08-NOV-1996;

(IDEC-) IDEC PHARM CORP

Hanna ď Brams Anderson DR,

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WPI; 1998-286601/25. P-PSDB; AAW63760.

New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between I and B cells, e.g. graft rejection or tumours

Example 7; Fig 3a; 87pp; English.

This sequence encodes a primatized form of the antibody 7010 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type in diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel diseases, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins anti-idiotype reagents.

or small molecule immunosuppressants Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses

Sequence 705 BP; 162 A; 214 C; 207 G; 122 T; 0 other;

Gaps · 0 Length 705; Indels 100.0%; Score 705; DB 19; 100.0%; Pred. No. 4.3e-167; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 705; Conservative

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2, 2003, 12:12:30 ; Search time 144.396 Seconds (without alignments) 13179.730 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.

Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idlopathic thromboytopeania purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type I diabetes mellitus; graft versus host disease;

hetero-hybridoma; transfectoma; ss

Chimeric Macaca cynomolgus; Chimeric Homo sapiens.

WO9640878-A1

19-DEC-1996.

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Shestowsky WS;

Brams P, Hanna N,

Anderson DR,

(IDEC-) IDEC PHARM CORP.

07-JUN-1995;

96WO-US10053. 95US-0487550

06-JUN-1996;

11 24 AAS17246 Primatised anti- 24 ABC76512 Human ovarian and ABC76512 Human cDNA encoding anti- 24 ABC86716 DNA encoding anti- 25 AAS2717 Human cDNA encoding and anti- 26 ABC57406 DNA encoding and anti- 27 AAS2777 Human cDNA encoding but and anti- 28 AAS2777 Human cDNA encoding but and anti- 28 AAS2777 Human cDNA encoding but and anti- 29 AAS2177 Human cDNA encoding but and anti- 20 AAS1344 Human cDNA encoding but and anti- 21 AAS1344 Human cDNA encoding but and anti- 22 AAS1344 Human cDNA encoding but and anti- 23 AAS3481 DNA encoding but and anti- 24 ABC8650 Human cDNA encoding but and anti- 25 AAS3481 Human cDNA encoding but and anti- 26 AAS3481 Human cDNA sequence encoding but and anti- 27 AAS87270 Human cDNA sequence encoding but and anti- 28 AAS887270 Human cDNA sequence encoding but and anti- 29 AAX06953 Monoclonal anti- 29 AAX06953 Human cDNA sequence conding but and anti- 20 AAX06953 Human cDNA sequence conding but and anti- 20 AAX06953 Human cDNA sequence conding but and anti- 21 ABC6418 Human cDNA sequence conding but and anti- 22 AAS887270 Human cDNA sequence conding but and anti- 24 ABC6418 Human cDNA sequence conding but and anti- 25 AAC64209 Human cDNA sequence conding but and anti- 26 AAC64209 Human cDNA sequence conding but and anti- 27 AAC64209 Human cDNA sequence conding but and anti- 28 AAC64209 Human cDNA sequence conding but and anti- 29 AAC64209 Human cDNA sequence conding but and anti- 20 AAC64209 Human cDNA sequence conding but and anti- 21 ABC6418 Human cDNA sequence conding but and anti- 22 AAC64209 Human cDNA sequence conding but and anti- 24 ABC64180 Human cDNA sequence conding but and anti- 25 AAC64209 Human cDNA sequence conding but and anti- 26 AAC64209 Human cDNA sequence conding but and anti- 27 AAC641800 Human cDNA sequence conding but and anti- 28 AAC641800 Human cDNA sequence conding but and anti- 29 AAC641800 Human cDNA sequence conding but and anti- 20 AAC641800 Human cDNA sequence conding but and anti- 21 ABC67100 Human cDNA sequence conding but and anti- 21 AAC641800 Hu	9 540.2 76.6 711 24 AAS17246 DNRP 11 527.6 76.4 711 18 AAT62112 HUN 12 52.6 76.4 711 18 AAT62112 HUN 13 520.6 73.9 904 24 ABS63438 HUN 14 520.4 73.9 904 24 ABS67760 DNRP 15 518 73.5 702 24 ABS67760 DNRP 16 518 73.5 702 24 ABS67760 DNRP 17 516.4 73.2 80. 24 ABS67760 DNRP 18 516.7 73.2 80.0 24 ABS67770 HUN 20 514.9 73.2 80.0 25 AAS2277 HUN 21 515.8 73.0 1825 22 AAS2277 HUN 22 512.8 72.7 960 21 AAC78188 HUN 24 72.7 960 21 AAC78188 DNRP 25 50.0 77.5 86.3 22 AAS33481 DNRP 26 50.0 77.5 86.3 24 AAS33481 DNRP 27 490 69.5 866 24 ABS63531 HUN 28 490 69.5 866 24 ABS63531 HUN 29 480 67.5 866 24 AAS33481 DNRP 29 480 69.5 866 24 AAS33481 DNRP 29 480 69.5 866 24 AAS33481 DNRP 29 480 69.5 866 24 AAS33481 DNRP 29 460 69.5 866 24 AAS33481 DNRP 29 462 65.0 826 22 AAC86525 HUN 29 462 65.6 915 24 AAB64815 HUN 20 462.8 65.6 915 24 AAB64815 HUN 20 462.8 65.6 915 24 AAB64815 HUN 21 462.2 65.5 8679 22 AAC84209 HUN 22 462 65.5 8679 22 AAC84209 BNA 24 66.8 65.6 915 24 AAB64491 HUN 25 66.9 826 55.5 8679 22 AAC84209 BNA 26 65.5 8679 22 AAC84209 BNA 27 462 65.5 8679 22 AAC84209 BNA 28 462.8 65.6 915 24 AAB6441 HUN 29 462.8 65.6 915 24 AAB6441 HUN 20 65.5 8679 22 AAC84209 BNA 21 462 65.5 8679 22 AAC84209 BNA 22 AAC84209 BNA 23 462.8 65.6 915 24 AAB6481 BNA 24 66.8 65.6 915 24 AAG9835 BNA 25 AAC84209 BNA 26 65.5 8679 22 AAC84209 BNA 27 66.8 65.6 915 24 AAB6481 BNA 28 462.8 65.6 915 24 AAG9835 BNA 29 462.8 65.6 915 24 AAG9835 BNA 20 462.8 65.6 915 24 AAG9835 BNA 20 462.8 65.6 915 24 AAG9835 BNA 21 462 65.5 869 22 AAC84209 BNA 22 AAC84209 BNA 23 AAC74209 BNA 24 662.8 65.6 915 24 AAG9835 BNA 25 AAC84209 BNA 26 65.5 869 25 BNA 27 AAC9800 BNA 28 AAC9800 BNA 29 AAC9800 BNA 29 AAC9800 BNA 20 BNA 20 BNA 21 AAC9800 BNA 22 BNA 23 BNA 24 BNA 25 BNA 25 BNA 26 BNA 27 BNA 28									
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Pred. No. is the number of results predicted by chance to have a

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Sequence 13547, A Sequence 13995, A Sequence 582, App Sequence 50, Appl Sequence 76, Appl Sequence 12838, A	sequence 42, Appl Sequence 1258, A Sequence 97, Appl Sequence 15, Appl Sequence 146, App Sequence 4, Appl	Sequence 5, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12799, A Sequence 31506, A	sequence 13206, Transquence 70, Appl Sequence 71, Appl Sequence 788, Appl Sequence 710, Appl Sequence 710, Appl Sequence 73, Appl Sequence 40, Appl
3-846- 301-5301-53- 3-846-	- 198 - 846 - 972 - 656 - 981 - 353 - 981 - 353 - 982 - 8492	-09-747-669- -10-290-703- -10-290-703- -10-198-846- -10-198-846-	846-13 646-7 646-7 646-7 1107-37 319-7 319-7 319-7 346-13
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520.8 516 512.8 510.6 510.6	0 00 7	44 444 472 472 472 472 472 674	4 4 6 5 8 4 6 5 8 4 6 6 3 8 4 6 6 3 . 2 8 6 6 2 . 8 6 6 2 . 6 8 6 6 2 . 7 6 8 6 7 6 6 7 6 6 6 6 6 6 6 6 6 6 6 6
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
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                                                                                                                                  E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         012712-131
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
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                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
             Darrell R.
                                                                                                                                                                                                                                                                 : Floppy disk
IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TRNGTH: 705 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
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                                                                                                 NUMBER OF SEQUENCES: 1
             Anderson,
                         TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                               705; Conservative
                                                                                                                                                                                                      mat_peptide
                                                                                                           MOLECULE TYPE: peptide
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US-09-948-429B-1
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107863 seqs, 158726573 residues
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                                                                                                                                         OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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Protein sequence o Ant-CD4 monkey-hum Monoclonal rabies Primatised anti-hu Macaque primatized Description AAU14924 AAU14924 ABU08020 ABG19295 AAG19299 AAU14412 AAW01817 8 Query Match Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody, Mab, macaque; light chain, primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/5 cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                      1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA
                                                                                                                                                                                                                                                                                                                                                                                                                               RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                          Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1243; DB 18; Length 234; 100.0%; Pred. No. 1e-70; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaque primatized 7C10 light chain protein.
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                                                                                 Claim 6; Fig 8A; 81pp; English.
                                                                                                                                                                                                                                                          and graft-versus-host disease,
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WPI; 1997-108638/10.
N-PSDB; AAT62509.
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This sequence represents a primatized form of the antibody 7C10 light chain from macaque. This sequence is used in a method which studies new moncolonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving really early inflammatory bardiants, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple solerosis, graft vs. Inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases. B cell lymphoma infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression and antigen-specific immunosuppression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; macaque monkey; light chain; primatised antibody; 7C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
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100.0%; Pred. No. 1e-70;
iive 0; Mismatches 0; Indels
                                                                                                                                 cells, e.g. graft rejection or tumours
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                                                                                                                                                                           Example 7; Fig 3a; 87pp; English.
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Chimeric - Macaca sp.
Synthetic.
WPI; 1998-286601/25.
N-PSDB; AAV35484.
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S25/50

Id lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22.Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: 525/56

B;Combriato, G; Klobeck, H.G.

Eur. J. Immunol.-21, 131-1522, 1991

A;Reference number: 816439; MUID: 91257162; PMID: 19044862

A;Reference number: 816439; MUID: 91257162; PMID: 19044862

A;Residue; preliminary; translation not shown

A;Residues: 1-23 < COMDA

A;Cross-references: EMBL:X57821; NID: 933741; PIDN: CAA40958.1; PID: 933742

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
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CiSpecies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiSpecies: SiSS547
Ricombriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) end gene segments of the human immunoglobulin A;Reference number: S16439; MuID:91257162; PMID:1904362
A;Accession: S25747
A;Status: preliminary; translation not shown
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81.7%; Score 1016; DB 2; Length 232;
Best Local Similarity 86.0%; Pred. No. 8.7e-61;
Matches 196; Conservative 14; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig lambda chain - human
C; Species: Homo sapiens (man)
C; Accession: S25753
R; Combriato, G; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A; Title: Vlambda) and J(lambda)-C(lambda) gene segments of the human immuno A; Title: Vlambda) and J(lambda)-C(lambda) gene segments of the human immuno A; Teference number: S16439; MUID: 91257162; PMID: 1904362
A; Status: preliminary; translation not shown
A; Residues: 1-231 <COM>
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R;Combriato, G:; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A;Title: V(lambda) and J(lambda) C(lambda) gene segments of the human immu A;Reference number: $16439; MUD: 91257162; PMID: 1904362

A;Accession: $25751

A;Accession: $25751

A;Residues: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-231 <COM>
A;Residues: 1-231 <COM>
A;Residues: 1-231 <COM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Superfamily: immunoglobulin homology <CMA>
F;146-214/Domain: immunoglobulin homology <CMA>
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79.0%; Pred. No. 5.3e-57;
iive 14; Mismatches 23
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hes 184; Conservative
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                                                                                                                                                                                                                                                                                                                               7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQRPARAPILV
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Ig lambda chain - human
Ig Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LLWLP-----GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR
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                                                   A)Cross-references: EMBL:X57812; NID:933723; PIDN:CAA40949.1; PID:933724 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;148-216/Domain: immunoglobulin homology <IXM>
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                                                                                                                                                                                                                      Length 233;
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.5e-60;
ss 20; :
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Pred. No. 2.5e-58;
                                                                                                                                                                                            81.5%; Score 1.5e-5
85.1%; Pred. No. 1.5e-5
13; Mismatches
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Best Local Similarity 85.1%
Matches 194; Conservative
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Best Local Similarity 80.38
Matches 187; Conservative
                            -233 <COM>
A; Molecule type: mRNA A; Residues: 1-233 <CO!
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MEDLINE-71150336; PubMed-5549568;
Ponstingl H., Hess M., Hischmann N.;
Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-protein Kern). V. The complete amino acid sequence and its genetic Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
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SEQUENCE (DOT).
MEDLINE-95255298; PubMed-7737190;
Stoppini M., Bellotti V., Negri A., Merligi G., Garver F., Ferri G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATIAL SEQUENCE (MYELOMA PROTEIN NEWM).
MEDLINE=74109253; PubMed=4814727;
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Anino acid sequence (the (lambda) light chain of a human myeloma immunoglobulin (tgG New).";
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SEQUENCE (BENCE-JONES PROTEIN SH).
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Titani K., Wikler M., Shinoda T., Putnam F.W.;
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10. CLEATED PR0423;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
19-SEP-2003 (Rel. 42, Last annotation)
19-SEP-2003
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MEDLINE-69088380; Pubmed-4883841;
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P01712
P01712
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MEDLINE-83186114; PubMed-6404900;
Kanetani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
  LV2F_HUMAN
LV6E_HUMAN
LV1F_HUMAN
LV2C_HUMAN
LV2E_HUMAN
LV2E_HUMAN
LV2E_HUMAN
LV2L_HUMAN
LV2L_HUMAN
LV2L_HUMAN
                                                                                                                                                                                                                                                    KV1X_HUMAN
LV2D_HUMAN
LV1_CHICK
     Shimizu A.;
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Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
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MEDLINE-90133913; PubMed-2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in where. Conformational flexibility of a molecule in two crystal forms.";
                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
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Obljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
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Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panagiotopoulos N.;
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                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
MEDINNE-75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
"Primary structure of the Mcg lambda chain.";
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EMBL, 138652; AAB5681.1; ALT_INIT.
EMBL, X51754; CA38569.1; ALT_INIT.
EMBL, X51755; CA36049.1; -
PIR, X51755; CA36051.1; -
PIR, X51757; CA36051.1; -
PIR, X92057; L2H0.
                           immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995)
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Genew; HGNC:5856; IGLC2.
Genew; HGNC:5857; IGLC3.
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GO:0006955;
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PDB;
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PDB;
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60;
REAL PROPERTY OF THE PROPERTY
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130 OPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                              Immunoglobulin C region; Bence-Jones protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Immunoglobulin lambda-like polypeptide l precursor (Immunoglobulin-related 141 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
IGLL1 OR IGL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McKearn J.P.;
"Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are expressed in pre-B cells and may encode the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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SEQUENCE FROM N.A.
MEDLINE-89315835, PubMed=2501791;
Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
McKearn J.P.,
McKearn J.P.,
                                                                                                                                                                                                                                                                   INTERCHAIN (WITH HEAVY CHAIN).
A -> N (IN MCG4 MARKER).
FTIG-VAR_003898.
S -> T (IN MCG4 MARKER).
FTIG-VAR_003899.
T -> K (IN KERN+ MARKER).
T -> K (IN MCG4 MARKER).
R -> K (IN 024 MARKER).
FTIG-VAR_003901.
R -> K (IN 024 MARKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSIVEKTVAPTECS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 SNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.1%; Score 548; DB 1; Length 10
100.0%; Pred. No. 7.6e-37;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11236 MW; DCD9C7C201C13CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig. 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; IRR; I.PROSITE; PS00290; IG_MHC; I.Mmunoglobulin domain; Immunoglobulin domain; Immunoglobul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 105; Conservative
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100
86
104
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DOMAIN
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P15814;
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DISULFID
VARIANT
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TURN
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ILL1_HUMAN
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081062 mus musculu 091w12 mus musculu 091w12 mus musculu 091w18 mus musculu 091w18 mus musculu 081c18 mus musculu 081c18 mus musculu 081c18 homo sapien 091c1 homo sapien 0951c1 homo sapien 0961c2 homo sapien 09054 ginglymosto 081c77 homo sapien 09051c mus musculu 080c91 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Straubbergary R.;
L Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
L Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC020990; AAR128090.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007359; Ig-c1.
R InterPro; IPR003596; Ig-w.
R InterPro; IPR003596; Ig-w.
R InterPro; IPR003596; Ig-w.
R SMART; SM00407; Ig; 2.
R SMART; SM00407; IG: 2.
R SMART; SM00409; IG-like; 2.
R PROSITE; PS5083290; IG_LIKE; 2.
R PROSITE; PS508320; IG_LIKE; 2.
R PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
R Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.4%; Score 1037; DB 4; Length 23
86.5%; Pred. No. 6.6e-83;
live 15; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
           Q8R062
Q91W12
Q91W87
Q91WF8
Q91WF8
Q8VC55
Q8R028
Q8R028
Q9NSD6
Q9NSD6
                                                                                                                                                      096JD0
096JD1
096JD2
081ZD8
096SB0
090SS4
090SS4
090SS4
090SS6
090SS6
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090SS4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.5%
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Brain;
08N355
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Q8N355
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sapien
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                                                                                  (without alignments)
2666.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     2, 2003, 08:56:23; Search time 22.6452 Seconds
                                                                                                             US-09-758-173-2
1243
1 MRVPAQLIGLILLMLPGARC........CQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8n355 homo s
Q8n5f4 homo s
Q8n5f4 homo s
Q8n4k4 homo s
Q8nuk4 homo s
Q8nuk1 homo s
Q8nuk1 homo s
Q8nuk3 homo s
Q8nuk3 homo s
Q9sml1 mus f
Q9sml1 mus f
Q9sml1 mus f
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Q8nek1 homo s
Q9d8w4 mus n
Q8nek0 homo s
Q8tcd0 homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBTCJ5
QBVCP0
QBNEK1
Q9DBW4
QBNEK0
QBNEK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8N355
Q8TBC9
Q8N5F4
Q96L69
Q8WTU6
Q8WTU6
Q96E61
Q99EK3
                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_organelle:*
sp_phage:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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Match 1
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                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymoraplans (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                 77.3%; Score 961; DB 4; Length 233; 80.3%; Pred. No. 3e-76; Live 16; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007782; AAH07110; 19-11ke.
R InterPro; IPR003006; 1g_MHC.
R InterPro; IPR003596; 1g_V.
R InterPro; IPR003596; 1g_V.
R InterPro; IPR001412; tRNA-synt_I.
R PRAMI; SM00406; IGV. I.
R PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
R PROSITE; PS00290; IG_LIKE; 2.
R PROSITE; PS00290; IG_MHC; 1.
R HYPOThetical protein.
SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 233 AA; 24961 MW; F092CFB6AA6E3A9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.8%; Score 917.5; DB 4; Best Local Similarity 78.1%; Pred. No. 1.9e-72; Matches 178; Conservative 17; Mismatches 32;
                                                         Strausberg R.;
Submitted (JUN-2002) to the EM
EMBL; BC032452, AAH31452.1;
InterPro; IPR003599; Ig_C1.
InterPro; IPR003599; Ig_C1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00356; Ig_WHC.
InterPro; IPR00356; Ig_V.
Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00409; IGC1; 1.
SMART; SM00406; IGC1; 1.
SMART; SM00406; IGC1; 1.
SMART; SM00406; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
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                                        62 APILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP-VFGGGTRV
                                                                                                   TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETITPSKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
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01-0CT_2002 (TrEMBLrel. 22, Last sequence update)
01-0CT_2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Elwano sapiens (Human).
Elwano sapiens (Human).
Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       186 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                     186 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC0223313. AAH22023.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_V.
Ffam: PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                      PRT;
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Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue=B-cell;
                                                                                                   126
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Query Match

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Q8TBC9; QBTBC9

RESULT :

181

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Q8N5F4 Q8N5F4;

RESULT 3 Q8N5F4

65

16, Appl 17, Appl 8, Appli 5, Appli 26, Appl 24, Appl 20, Appl

Sequence 1 Sequence 8 Sequence 8 Sequence 5 Sequence 2 Sequence 2

Sequence 153, App Sequence 153, App Sequence 153, App

Sequence 153,

4, Appli 2, Appli

Sequence Seq

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Sequence 2, Application US/08487550
Patent No. 6113891
Patent No. 6113891
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE DE INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVPAQLLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN 1995
ATONREY/AGNET INPORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
RESPERENCE/DOCKET NUMBER: 35,030
REJERRATION NUMBER: 35,030
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 703-836-6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1243; DB 3;
100.0%; Pred. No. 1.2e-102;
ive 0; Mismatches 0;
US-08-812-586-16
US-09-53-53-81
US-09-53-53-81
US-09-140-002-26
US-09-740-002-24
US-09-740-002-24
US-09-740-002-24
US-09-740-002-24
US-08-899-575-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100. les 234; Conservative
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    ; MOLECULE TYPE: protein US-08-487-550-2
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  USA
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Best Local S
Matches 234
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Sequence 2, Appli
Sequence 6, Appli
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Appl
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Sequence 56, Appl
                                                                                                                          2003, 09:12:09; Search time 10.3927 Seconds (without alignments) 952.662 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22,
Sequence 51,
Sequence 9, Ar
Sequence 9, Ar
Sequence 9, Ap
Sequence 6, Ap
Sequence 6, Ap
Sequence 14, Ap
Sequence 14, Ap
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Sequence 10, A
Sequence 10, A
Sequence 4, Ap
Sequence 7, Ap
Sequence 12, Ap
Sequence 22, Sequen
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1243
1 MRVPAQLLGLLLLWLPGARC......CQVTHBGSTVEKTVAPTECS
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/cgn2_6/ptcdata/1/laa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/laa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/laa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/laa/PCTUS.COMB.pep:*
/cgn2_6/ptcdata/1/laa/PCTUS.COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-422-112-9
US-09-313-942-14
US-09-025-769B-170
US-07-916-098A-56
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US-09-526-098-2
US-08-487-586-10
US-09-526-098-10
US-09-0425A-4
US-09-049-672A-1
US-08-049-672A-11
US-09-049-672A-11
US-09-049-672A-11
US-09-049-672A-12
US-09-049-672A-12
US-09-049-672A-12
US-09-049-672A-12
US-09-152-060-88
US-09-152-060-88
US-08-977-146-22
US-08-977-146-22
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Maximum Match 100%
Listing first 45 summaries
                                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Maximum DB :
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Gaps

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Length 234; Indels

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127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV
                                                                            181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                        Patent NO. DIJULE.
GENERAL INFORMATION:
GENERAL Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKOSNNKYAASSYLSLTPEQWKSHRSYSCOVTHEGSTVEKTVAPTECS 234
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Pred. No. 1.7e-82;
0; Mismatches 21; 1
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                                                                                                                                                                                                                                                                                                                                            BURNS, DOANE, SWECKER & MATHIS
699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
APPLICATION UNMER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                        Sequence 6, Application US/08523894
Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.7%;
86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22314:3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.0
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 233 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: protein US-08-523-894-6
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-08-487-550-10
                                                                                                                                                        US-08-523-894-6
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                   GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                                                   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
                                                                                                                                VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                   Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 4;
1.2e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: BURNS, DOANE, SWECKER & MATHIS: 699 Prince Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1243;
100.0%; Pred. No. 1.5
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                 Sequence 2, Application US/09526098
Patent No. 6492134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: US OF FILING DATE: 07-JUN-1995
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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APPLICANT: Anderso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
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Best Local Simi
Matches 234;
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CITY: Al
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US-09-948-429B-2
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STATE:
                                                                                                               2, 2003, 09:18:44; Search time 87.8457 Seconds (without alignments) 421.442 Million cell updates/sec
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1243
1 MRVPAQLLGLLLLWLPGARC.......CQVTHEGSTVEKTVAPTECS 234
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/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_USW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10B_PUB.puB.pep:*
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/ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ggn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ggn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-124-807-2
US-10-211-357-6
US-10-211-357-6
US-09-972-656-96
US-09-972-656-96
US-10-124-807-10
US-10-124-807-10
US-10-124-807-10
US-10-124-905-10
US-10-124-905-10
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US-09-972-11-134-51
US-09-972-656-98
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                                                                                                                                                                                                                                                                                                                                           587654 seqs, 158212981 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications AA:
                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2 US-10-225-108A- 1 US-09-972-656-1 2 US-10-194-801C- 0 US-09-747-669-6 0 US-09-747-669-6 4 US-10-001-857-2- 1 US-09-972-656-8	0 US-09-974-449-3 1 US-09-972-656-9 1 US-09-972-656-1 2 US-10-076-747-8 2 US-09-853-161-70 US-09-852-659A-7 0 US-09-852-797-7	S. 09-852-759A S. 09-852-759A S. 09-7362-731 S. 09-828-955 S. 09-909-567 O9-291-299A -09-291-299A -09-291-299A -09-291-299A S. 09-796-692 S. 09-796-692 S-10-040-862
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ALIGNMENTS

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Gegenence 2. Application US/09948429B

Sequence 2. Application US/09948429B

Patent No. US20020177699A1

Patent No. US20020177699A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PRARAACETIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS INTER OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: BACKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STREET: VA

COUNTY: Alexandria

STREET: BW PC Compatible

COUNTY: Alexandria

STREET: BW PC COMPATIBLE

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CORRESPONDENCE: Patentin PC-DOS/MS-DOS

SOFTWARE: Patentin PC-DOS/MS-DOS

SOFTWARE: Patentin PC-DOS/MS-DOS

SOFTWARE: PAPLICATION NUMBER: US 09/383,916

FILING DATE:

FILING DATE:

REPERRORS/ACRATION NUMBER: 35,030

RESISTRATION NUMBER: 35,030
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US-10-2030180290a1

US-10-203018020a1

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                                                                                                                                                Length 234;
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4.8e-92;
0;
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100.0%; Pred. No. 4.8e-92;
Live 0; Mismatches 0;
                                                                                                                                       100.0%; Score 1243;
100.0%; Pred. No. 4.8
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 234; Conservative
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                                 TOPOLOGY: linear
                                                            ; MOLECULE TYPE:
US-10-124-807-2
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BORNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITT: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1243; DB 10; Length 234;
100.0%; Pred. No. 4.8e-92;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-124-807-2
Sequence 2, Application US/10124807
Publication No. US20030166207A1
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELEFAX: 703-830-20-2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TYPE: linear
                                                                                                                                                                                                                                                                                                         Best Local Similarity 100. Matches 234; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds (without alignments) 15574.362 Million cell updates/sec
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1431
1 ATGAAACACCIGIGGTICTI.......CCCIGICICCGGGTAAAIGA 1431
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                          2888711 seqs, 20454813386 residues
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Listing first 45 summaries
                                                  OM nucleic - nucleic search, using sw model
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

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us-09-758-173-3.rge

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BASE COUNT ORIGIN	organ 322 a 46	ପ୍	961 GGGGAGGAGTACAGCACGTACCGTGTGTGTGTGTGTGTGT	
Query M Best Lo Matches	y Match 100.0%; Score 1431; DB 6; Length 1431; Local Similarity 100.0%; Pred. No. 3.6e-278; hes 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	δδ ·	1021 GACTGGCTGAATGGCAAGGAGTACAAGTCTCCAAGAAAGCCTTCCAGCCCCCCCC	
oy Dp	ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCC 	<i>장</i> 집	1081 ATCGAGAAAACCATCTCCAAAGGCCAGGCCCCGAGAACCAGGTGTACACCTG	
් ර සි	GIGAAGCIGCAGCAGGGGGGAAGGACTICGGGGGCGTGGGGGGCGTGGGGGGGGGG	a S	1141	
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oy Db	81 CCAGGGAGGGACTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 24	δ.	1261 AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC 1	
Qy	241 AATCCCTCCTCAAGAGTCGAGTCACCATTCAAAAGACAGTCCAAGAACCAGTTCTTC 300 	& A	1321 GIGGACAAGAGCAGGIGGAACAGGGGAACGICITCICATGCICCGIGAIGAAGI	
Qy Dp	CTGAACTTGAATTCTGTGACCGACGGGGCGCCGTCTATTACTGTGCGAGAG 	g da	1381 CTGCACAACCAGCAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1431	
QY Db	361 CGCCCTGAITGCACAACCAITTGITATGGCGGGCTGGGTCGATGTCTGGGGCCCGGGAAC 420 		AR265197	
Qy Db	421 CIGGICACCGICICCICAGCIAGCACCAAGGCCCCAICGGICITCCCCCTGGCACCTIC 480		TION Sequence 3 Irom parent US 04921 ION AR265197 DS AR265197 1 GI:29693618 DS	
Qy Db	481 TCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCC 540	<i>σ</i> , <u>μ</u>		
QY Db	541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG 600		Ċ	
Qy Db	601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660	щО	SOUICE 1.1431 Aorganism="unknown" BASE COUNT 322 a 469 c 380 g 260 t	
Qy Db	661 AGCTIGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720 		Query Match Best Local Similarity 100.0%; Pred. No. 3.6e-278; Length 1431; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Qy Db	781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTC 840 	О П	Oy 61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCGGCACC 120	
Q7 Dp	841 ATGATCTCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAGACCCT 900	<u> </u>	09 121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTACTGGACCTGGATCCGCCAGACC 180	
Qy Db	901 GAGGTCAAGTTCAACTGGTAGGAGGGGGTGGAGGTGCATAATGCCAAGACAAAGCG 960 	<u> </u>	OY 181 CCAGGAGGGACTGCAGTGGATTGGCCATATTATGGTAATGGTGCGACCACCTAC 240	

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2, 2003, 12:12:30 ; Search time 293.094 Seconds (without alignments) 13179.730 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Primatised anti-hu	Macaque primatized	DNA sequence of a	Primatised anti-hu	Macaque primatized	DNA sequence of a	Human immune syste	Monoclonal antibod
CHANNELLOC			ID ID	AAT62510	AAV35485	AAS17243	AAT62513	AAV35489	AAS17247	AAZ50012	AAT18059
			DB	18	13	24	æ ⊢1	19	24	21	17
			Match Length DB ID	1431	1431	1431	1431	1431	1431	1634	1431
	ф	Query	Match	100.0	100.0	100.0	91.9	91.9	91.9	87.1	86.5
			Score	1431	1431	1431	1315.8	1315.8	1315.8	1246.4	1237.2
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7 22 AAC66522 8 117 AAT628689 4 118 AAT628670 4 128 AAT628670 8 22 ABT14317 8 12 AAH746870 0 24 AAR12855 7 12 AAC88701 7 24 AAT12855 7 12 AAC8820 8 21 AAC820 1 22 AAC820 1 22 AAC820 1 12 AAC820 1 12 AAC820 1 12 AAC820 1 13 AAC820 1 14 AAC820 1 14 AAC820 2 24 ABE66479 2 24 ABE66479 2 24 ABE66479 3 24 ABE66479 6 24 ABE66479	00000000000000000000000000000000000000	1431 BP. Y) I antigen antiboc omolgus monkey; me antigen; CD28; imm pathic thrombocytc osus; rheumatoid a sus; rheumatoid a sctoma; ss. us; 1431 BP. I antigen antiboc of a configuration of a configuration of a cotoma; ss. Us; 1550.
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Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
                                                                                         TTCTATCCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAGCCGGAGAACAACTAC
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/product= 7C10 heavy chain
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                                                                Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
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P-PSDB; AAW01818.
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		http	Liang 1	Length	inv	itrogen.com/ 8	VitroGen	Corporation	1600
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Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 9106 EVRY cedex - France

Library was, constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq-CS0CAP001AE07NP18cluster=7198.r. Contact:

Feng Liang Email: fliang@llfetech.com URL:

Feng Liang Email: fliang@llfetech.com URL:

Franday Avenue Genoscope sequence ID: CS0CAP001AE07NP1.
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/wol_type="mRNA"
/wol_type="mRNA"
/db.xref="taxon:9606"
/clone="type="THYMUS"
/tissue_type="THYMUS"
/clone_lib="Homo saplens THYMUS"
/note="Vector: pcMVSPORT_6; 1st strand cDNA was primed
/with a NotI-ollgo(dT) primer. Five prime end enriched,
with a NotI-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Iithrary was not normalized."
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                                                         ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1297
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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343 GCCTGACCTGCTCGAAGGCTTTATCCCAGCGACATCGCCGTGGAGTGGGAAGCA
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                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs01009v10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
siles of the pcNVSPORT 6 vector. Library was normalized.
296 c 396 g 267 t cthers
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                                                                                                                                                                                                                                                                                                                                                                                                         398 TCGATGTCTGGGGCCCGGGAGACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCAT
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      Avenue Genoscope sequence ID : CSODI009DE05NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Length 1201;
                                                                                                                                                                                                                                                                                                                          66.0%; Score 944; DB 13; 95.8%; Pred. No. 8.8e-198; tive 17; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                       991; Conservative
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Sequence 3, Application US/08487550

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GENERAL INFORMATION:
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MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                             US-09-343-485A-3

US-08-378-939-9

US-08-378-939-9

US-09-027-449-68

US-09-027-4449-68

US-09-121-952A-68

US-09-121-952A-68

US-08-137-101A-68

US-08-149-099C-3

US-08-149-099C-3

US-08-1476-275-2

US-08-4778-915-3

US-08-4778-915-3

US-08-4778-915-3

US-08-4778-915-3

US-08-478-915-3

US-08-478-915-3
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NAME: Teskin, Robin L.
REGISTRATION UNDRER: 35,030
REFERENCE/COCKET UNDRER: 01271
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-6620
TELEFAX: 703-836-62021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
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COUNTRY: USA
ZIP: 22314
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LOCATION:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-526-098-3
US-08-427-550-11
US-09-626-098-11
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US-08-523-894-7
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US-08-488-376-17
US-08-634-224-17
US-08-634-224-17
US-08-634-21-17
US-08-634-81-17
US-09-335-6978-17
US-09-335-6978-17
US-09-335-6978-17
US-09-340-002-17
US-09-740-002-17
US-09-140-002-17
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US-08-488-376-19
US-08-634-223-19
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US-09-335-697B-19
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1021 1081 1141 1141 1201	AGGCT 1	RESULT 2 US-09-526-098-3 Sequence 3, Application US/09526098 - patent No. 6403134	DAIRELL R. "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS	TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF; TITLE OF INVENTION: IMMUNOSUPPRESANTS"; NUMBER OF SEQUENCES: 12 ; CORRESPONDENCE ADDRESS: ADDRESSER: BIRNS, DOANE, SWECKER & MATHIS	ð	COMPANY 22314 ZIP: 22314 COMPUTER READABLE FORM: MEDIUM TYPE: Florby disk	COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS COFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	APPLICATION NUMBER: US/09/526,098 FILING DATE: CLASSIFICATION: FRICR APPLICATION DATA:	APPLICATION NUMBER: 09/383,916 FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-111N-1995	ATTORNEY/AGENT INFORMATION: NAME: Teskin, Robin L. REGIETRATION UNDRER: 35,030	ATION:	101	; STRANDEDNESS: NOT FELEVANC; TOPOLOGY: linear ; MOLECULE TYPE: peptide
Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATGAAACACCTGTGGTTCTCCTCTGTGGCAGTTCCTCTGTGGGGTCCTGTCCGG 0 1	QY 181 CCAGGAGGGACTGGAGTGGCATATTTATGGTAATGGTGACCACCAACTAC 240 Db	Db 301 CTGAACTIGAATTGTGACCGACGCGACACGCCGTTATTACTGTGTGTG	421 CTGGTCACCGTCTCAGCTAGCACCCAGGGCCCATCGGTCTTCCCCTGGCACCCTCC	481 481 541	541 GAACCGGTGACGGTGTGGTGAACTCAGGCGCCTGACCAGGCGTGCACCTTCCCG [OY 001 GCIGICCTACABICCTCASSACTCTACTCASCASSCOTSGIGACCGIGCCTCCASC 000	QY 661 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACCACCAAGGTG 720 DD 1 1 1 1 1 1 1 1 1 1	OY 721 GACAAGAAAGCGAAATCTTGTGACAAAACTCACACTGCCCACGTGCCCAGCA 780	Oy 781 CCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCTC 840	0y 841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAACACCCT 900 11	DY 901 GAGGTCAAGTTCAACTGGTACGTGGCGTGGAGGTCCATAATGCCAACACAAAGCCG 960 111111111111111111111111111111111111	Qy 961 CGGGAGGAGCAGTACAACAGCTACGGTGAGCGTCCTCACCGTCCTGCACCAG 1020	Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCC 1080

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Description	Sequence 3, Appli Sequence 3, Appli	, w v	Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl	11,	Sequence 11, Appl Sequence 9, Appli Sequence 40, Appli Sequence 17, Appli Sequence 11, Appli
SUMMARIES	US-09-948-429B-3 US-10-124-807-3 US-10-291-532-3	US-10-124-905-3 US-10-073-138-2	US-09-948-429B-11 US-10-124-807-11 US-10-291-532-11	US-10-124-905-11 US-10-073-138-6 US-10-211-357-7	US-10-211-35/-11 US-10-211-35/-9 US-10-203-754A-40 US-09-740-002-17 US-10-225-108A-1
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1090	9.	76.2	8120	11	09-726-	9
1089	7	76.1	1356	10	9-822-	N
1088.	ω.	76.1	1539	σ	-09-822-84	Sequence 87, Appl
1087	9.	76.0	1615	σ	9-822-84	Sequence 111, App
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ALIGNMENTS

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TITLE OF INVENTION: DANE, SWECKER & MATHIS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: DANE, SWECKER & MATHIS CONTAINING, AND USE THEREOF STREET: 699 Prince Street

CITY: Alexandria STREET: 699 Prince Street

CITY: Alexandria STREET: GOOMPUTER: IEM PC COMPATABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PLOPPy disk COMPUTER: PLOPPy disk COMPUTER: PLOPPY DATA: DELGATION DATA: DELGATION NUMBER: US/09/948,429B

FILING DATE: 07-JUN-1995

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Sequence 3, Application US/10124807

Publication No. US20030166207A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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ZIP: 22314
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MEDIUM TYPE: Floppy
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100.0%; Score 1431;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1431; Conservative 0; Mismatches
                                                                    not relevant
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:-
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
                                                  TYPE: nucleic acid
STRANDEDNESS: not rele
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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1..1431
                                                                                                                                  NAME/KEY:
LOCATION:
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US-09-948-429B-3
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Human immunoglobul

Reshaped CAMPATH-1

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Mus musculus antiMus musculus antiLight chain amino
Anti-Ige antibody,
Full length heavy
Full length heavy
Human C5E10 antibody C5E10 hea
Human E27 anti-IgE
Mus musculus anti-

Scoring table:

Searched:

Database

Sequence:

Title:

on:

Run

Amino acid sequenc E27 anti-12E antib Full length heavy Humanised 1D10 ant Humanised 1D05 ant Human anti-RSV mon Protein #2 in inve

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Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idlopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primatised anti-human B7.1 antigen antibody 7C10 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                        AAB26884
AAR22757
                                                                                                     AAB81972
AAR22759
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AAW95659
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AAW95663
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AAB76952
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                        AAW01818;
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AAW01818
ID AAW0.
 % Search time 55.856 Seconds
(without alignments).
1352.654 Million cell updates/sec
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2: /SIDSI/goddata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/goddata/geneseqy-embl/AA1981.DAT:*
4: /SIDSI/goddata/geneseqy-embl/AA1983.DAT:*
5: /SIDSI/goddata/geneseqy-embl/AA1983.DAT:*
5: /SIDSI/goddata/geneseqy-embl/AA1986.DAT:*
6: /SIDSI/goddata/geneseqy-embl/AA1986.DAT:*
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7: /SIDSI/goddata/geneseqy-embl/AA1997.DAT:*
8: /SIDSI/goddata/geneseqy-embl/AA1997.DAT:*
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2577
1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476
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                                                                                                                                                                                                                                                                   1107863
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                         1107863 seqs, 158726573 residues
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Humanised MaEll Ve Heavy chain amino Primatised anti-hu Human C2B8 antibod Antibody C2B8 heav

Shestowsky WS;

Hanna N,

Brams P,

Anderson DR,

(IDEC-) IDEC PHARM CORP.

Macaque primatized Protein sequence o Primatised anti-hu Macaque primatized Protein sequence o Human immune syste Human immune syste Monoclonal antibod

AAW63761 AAU11539 AAW01822 AAW63765 AAU11646 AAU11646 AAE336206 AAY44721

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21 m 4 m 20 r 20 q

Primatised anti-hu

AAW01818

Result

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96WO-US10053 95US-0487550

06-JUN-1996; 07-JUN-1995;

Macaque primatized Protein sequence o

Sequence of

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Hanna

PHARM CORP Brams P,

(IDEC-) IDEC Anderson DR,

08-NOV-1996;

97WO-US19906 96US-0746361

29-OCT-1997; 14-MAY-1998

proliferation;

T cell

Macaca fascicularis

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                                                                                                                            2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomologus monkey anti-human B7.1 antigen monoclonal antibody 7010. Cloned 7010 light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into variable genes (see also AAT62509 and AAT62510) are inserted into variable genes (see also AAT62509 and AAT62510) are inserted into variable years of pref. NEOSLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGRGLEWIGHIYGNGATTNYNPSLKSRVIISKDISKNOFFLNLNSVIDADIAVYCARGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                 tch 100.0%; Score 2577; DB 18; Length 476; al Similarity 100.0%; Pred. No. 1.3e-146; 476; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primatized 7C10 heavy chain DNA.
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                                                                                              6; Fig 8B; 81pp; English
                                                                                                                                                                                                                                                                                                    and graft-versus-host disease,
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This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new manoclonal antibodies (MAD's) that bind selectively to BT.1 (CD80) or to BT.2 (CD86) antipons and inhibits binding of these antiqens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically confidentiate thrombocytopaenia purpura, systemic lupus erythematosus, type of dispethic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sciencisis, aplastic anaemia, const diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small modecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and this immunosuppression, i.e. it inhibits contingen specific immunosuppression.
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                                                                                                                                                                                                                                                                                                                                                       New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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Matches 476; Conserv
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 2, 2003, 09:07:34; Search time 20:9182 Seconds
(without alignments)
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	2188.349 Million cell updates/sec
Title: Derfect score.	US-09-758-173-4 2577
Sequence:	1 MKHLWFFLLLVAAPRWVLSQMHEALHNHYTQKSLSLSPGK 476
Scoring table: BLOSUM62	BLOSUM62
	Gapop 10.0 , Gapext 0.5
Searched:	283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:	283308
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

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PIR_76:*	: pir1:	ir	: pir3:	4: pir4:*
Database :				

Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and is derived by analysis of the total score distribution.
Pred. No. is the number of	score greater than or equal	and is derived by analysis (

	Description	chain	chain	chain		chain	ain pr	chai	ū	Ig gamma-2a chain	ø	_	Ig gamma-2b chain	_	Ig gamma 2a chain	Ig gamma-1 chain C	Ig gamma 2b chain		Ig gamma 1 chain c	ain C		chain	ain C	Ig gamma-3 heavy c	chain		chain		chain	Ig gamma-3 chain C
SUMMARIES	QI	СННО	A23511	A60764	GZHU	G4HU	S22080	S31459 ·	869339	S374B3	PC4436	\$40295	G2MS11	S01321	147159	S31866	147160	PT0207	147158	GHRB	I47161	G2GP	C30554	G3HUWI	PS0017	PS0018	G1MS	G3MSC	GIMSM	G3MSM
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G2MSA G2MSAB	G2MSAM S00847 PS0019	S06611 G2MSBM	147162 S38864	A49444 S04845	S25705 B46529	514683	S69340 S69131
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1122	1117 1114.5 1108	1088.5	1062 908	903 794.5	771	719	709.5
30	2 2 2 4 2 2 4	35.	38	39	417	43	44 45

ALIGNMENTS

RESULT 1 GHING THE Creation - human If gamma-1 chain C region - human C Species Home applaines (mai) C Species 13-748-1991 Essequence_revision 16-Aug-1982 #text_change 16-Jul-1999 C Accession A343-35.8661; 833667; 890663; 890664; 891668; A91723; A02146 R.Ellison, J. W.; Besson, B. J.; Hood, L. E. A.Accession: A343-35.8661; 833667; B00663; A90564; B91668; A91723; A02146 R.Ellison, J. W.; Beschence of a human immunoglobulin C-gammal gene. A.Accession: A343-35 A.Accession: A343-35 A.Accession: A343-35 A.Accession: A343-35 A.Accession: A343-35 A.Accession: A343-35 A.Accession: S5661. E. Ball, Z17370 A.Note: Lils Sequence has the Glu(17) allotypic marker, 97-Lys, and the Glm(1) marker R.Harris, L.J. B. Ball, Z17370 A.Note: Lils Sequence has the Glu(17) allotypic marker, 97-Lys, and the Glm(1) marker R.Harris, L.J. A.Accession: S5661. A.Accession: B9653. A.Accession: B9654. A.Accession: B9654. A.Accession: B9654. A.Accession: B9656. A.Accession: B9659. A.Acce	A; Residues: 136-154, 'Q', 156-165, 'Q', 1171-176, 'Q', 178-194,' N', 196-197,' D', 199-238, 'E', Z. A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R; Ponsting1, H.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976 A; Title: Die Primaerstruktur eines monoklonalen 19G1-Fmmunglobulins (Myelomprotein Ni
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Accession: A23511

R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Accession: A23511
R; Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1799-1789, 1986
A; Title: Sequence of a human immunoqLobulin gamma 3 heavy chain constant region gene: A; Reference number: A23511; MUID:86148507; PMID:3081877
A; Recession: A23511
A; Molecule type: DNA
A; Residues: 1-377 <HUC>
A; Residues: 1-377 <HUC>
C; Genetics:
A; Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C; Genetics:
A; Gene: GDB:IGHG3
A; Map position: 14432.33-14432.33
A; Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C; Superfamily: immunoglobulin c region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u) with an IGHG4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47;
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 81.7%; Pred. No. 5.2e-89;
Matches 308; Conservative 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: protein
A, Molecule type: protein
A, Residues: 1-96, Xr, 98-197, D', 199-238, YE', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A, Residues: 1-96, Yr', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A, Rote: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.', Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUID: 71064027; MUID: 4923144
A; Contents: annotation: disulfide bonds
A; Contents: sunctation: disulfide bonds
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Reference number: A91667; MUID: 77070267; PMID: 1002129
A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A map position: 1493.33-14932.33
A; introns: 99/1; 114/1; 224/1
A; introns: 114/1; 224/1
A; introns: 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114
                                                                                                                     A; Molecule type: protein
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A; Residues: 1.34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Residues: 1.34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', '199-238, 'D', 240, 'L', '242-268, 'E', 27
A; Note: this sequence has the Glm(17) and Glm(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOI
A; Reference number: A91723; MUID: 83289131; PMID: 6884994
A; Accession: A91723
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                    A)Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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A;Cross-references: GDB:120085; OMIM:147100
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                       OM protein - protein search, using sw model
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Run on: October 2, 2003, 08:56:23; Search time 13.1295 Seconds (without alignments)
1704.917 Million cell updates/sec
Title: US-09-758-173-4
Perfect score: 2577
Sequence: 1 MKHLWFFILLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P01857 homo sapien	OHOU	orycto	cavia p	homo s	rattus	rattus	gnw	snu	SIL	mus	ន្ទាយ	mus	¤ns wns	rattus	ratt	mus	m som	homo sa	rattus	homod	mus n	рошоц	น รกพ	oryc		oryctol	sunca		mesoc	P04220 homo sapien	heter
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ALIGNMENTS

RESULT 1 GC1_HUMAN 11D GC1_HUMAN POT 21-J DT 21-J CGN CAL CGN CAL CON CON CON CAL CO
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MEDILINE=77070257; PubMed=1002129;

MEDILINE=77070257; PubMed=1002129;

Dreker L., Schwarz J., Reichel W., Hilschmann N.;

Rule of antibody structure. The primary structure of a monoclonal 1931 immunoglobulin (myeloma protein Nie), I: Purification and Characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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GO; GO:0005823; F:antigen binding activity; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003097; Ig-c1.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00047; Ig; 3.
SWART; SW0047; IgC. 12.
PROSITE; PS00290; IG-MHC; 2.
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MEDLINE-81208100; PubMed-7236608;
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Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PDB, 1A77, 12-NDC-97.
PDB, 1D5B, 09-FEB-00.
PDB, 1D5V, 04-0CT-00.
PDB, 1DKV, 04-0CT-00.
PDB, 1E4K, 06-JUN-01.
PDB, 1E4K, 06-JUN-01.
PDB, 1EXC, 20-JUL-95.
PDB, 1TZ, 16-ANY-01.
PDB, 1IX, 16-ANY-01.
PDB, 1IX, 16-ANY-01.
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K -> R (IN GIM(3) MARKER).
/FTIGA-VAR_003886.
D -> E (IN GIM(NON-1) MARKER).
/FTIGA-VAR_003887.
L -> M (IN GIM(NON-1) MARKER).
/FTIGA-VAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN).
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_archeap:*

sp_vertebrate:* sp_bacteriap:*

sp_rodent:*

sp_virus:*

sp_fungi:* sp_human:* sp_invertebrate:*

sp_archea:*
sp_bacteria:*

sp_organelle:*sp_phage:*

sp_mammal:* sp_mhc:*

Description	Q8tc77 homo sapien Q8tc63 homo sapien Q8tc63 homo sapien Q8n49 homo sapien Q8n417 homo sapien Q81379 mus musculu Q99131 mus musculu Q99131 mus musculu Q991144 mus musculu Q99125 mus musculu Q99125 mus musculu Q99124 quos musculu Q991144 quos sapien Q95n34 equus cabal
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ALIGNMENTS

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64 LEWVSSMSSSSSTIYYADSVKGRFTISRDNAKNSLYLQMN6LRAEDTAVYXCARDLR-QL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 WVF--LVAILEGVQCEVQLVESGGGLVKFGGSLRLSCAASGFTFSS-YSMNWVRQAPGKG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQTPGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Gaps
                                                                                                                                 01-JUN, 2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Evkaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Eutheria; Primates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.2%; Score 2041.5; DB 4; Length 471; Best Local Similarity 82.8%; Pred. No. 1.7e-164; Matches 391; Conservative 22; Mismatches 52; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO24489; AAH24289.1;
Interpro; IPR007110; 19-11ke.
Interpro; IPR00306; 1g_MHC.
Interpro; IPR003566; 1g_V.
Pfam; PF00447; 19; 4.
PROSITE; SM00406; 1G_LIKE; 4.
PROSITE; PS00250; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                        471 AA.
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Spleen;
                                                                                                  Q8TC77
RESULT 1
Q8TC77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
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                                                                                                                                                      SO DER READER KENN KWENN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΫ́
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TISSUE-Primary B-Cells from Tonsils;
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SMART; SMO0407; 1Gc1; 3.
SMART; SMO0406; IGc1; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 368; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. Homo sapiens (Human).
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Q8N4Y9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 TPGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 PPGKGLEWIGTINFSG-NMYYSPSLKSRVTWSADMSENSFYLKLDSVTAADTAVYYCAAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 PRPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEADTH HILLING HEADTH HILLING HEADT HILLING HI
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                                                                                                                                                                                                   185 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA 244
                                                                                                                                                                                                                                                                                                                                                                                            EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSI-SGYYYWTWIRQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 471
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.

REMEL; BC025985; AAH25985.1; -
InterPro; IPR007010; Ig-11ke.

RINTERPRO; IPR007010; Ig-11ke.

RINTERPRO; IPR00306; Ig-W.

RINTERPRO; IPR003096; Ig-W.

REMRI; SM0406; IGY, 1.

REMSITE; PS00196; COPPER BLUE; 1.

REMSITE; PS00196; COPPER BLUE; 4.

REMSITE; PS00296; IG_HKE; 4.

REMSITE; RS00290; IG_HKE; 4.

REMSITE; RS00290; IG_HKE; 3.

REMSITE; RS00290; IG_HKE; 3.

REMSITE; RS00290; IG_HKE; 4.

REMSITE; RS00290; IG_HKE; 3.
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01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-JUN-2003 (TIEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Matches
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240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031178; AAH33178.1;
InterPro; IPR001397; 1g-11ke.
InterPro; IPR003997; 1g-0.1
InterPro; IPR003066; 1g_MHC.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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952.662 Million cell updates/sec
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Sequence 8, A
Sequence 7, A
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Sequence 18,
                                                                 October 2, 2003, 09:12:09 ; Search time 21.1407 Seconds
                                                                                                                               1 MKHLWFFLLLVAAPRWVLSQ.......MHEALHNHYTQKSLSLSPGK 476
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Sequence 14,
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Seguence 12
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Sequence 8,
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Sequence 1
Sequence 1
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Sequence 1
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-526-098-4
US-09-526-098-12
US-09-526-098-12
US-09-528-994-12
US-08-53-894-8
US-08-53-894-18
US-08-53-894-10
US-08-53-894-10
US-08-53-894-10
US-08-987-352B-14
US-08-987-352B-14
US-09-109-207C-14
US-09-109-207C-14
US-09-109-207C-18
US-09-109-207C-18
US-09-109-207C-18
US-09-296-005-18
US-09-296-005-18
US-09-282-866-2
US-09-283-866-2
US-09-283-866-2
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                                                                                                                                                                                     328717 seqs, 42310858 residues
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                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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                                                                                                                                                                                                                                length: 0
length: 2000000000
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2577
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Match Length
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Sequence Sequence Sequence S

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Sequence 4, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
ADNOR B7 2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2577; DB 3;
100.0%; Pred. No. 4.6e-206;
ative 0; Mismatches 0;
US-08-466-151-8

US-09-466-163B-8

US-09-026-985-71

US-09-026-985-71

US-09-234-340A-71

US-09-234-340A-71

US-09-68-37-2

US-09-68-37-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-148-7

US-09-148-7

US-09-148-7

US-09-148-7

US-09-148-7

US-09-148-7

US-09-301-593-30

US-09-301-593-30

US-09-301-593-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                   ALIGNMENTS
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION POR SEQ ID NO: 4: SEQUENCE CHRACTERISTICS: LENGTH: 476 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-487-550-4
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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012712-131
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                          Matches 476; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   MOLECULE TYPE: protein
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                                                     Query Match
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US-08-487-550-12
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US-09-526-098-4
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Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS*
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 PGRGLEWIGHIYGNGATINYNPSLKSRVTISKDTSKNOFFLNLNSVTDADIAVYYCARGP 120
                                                                                            241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                                              PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                        RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                               EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                                           EVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLIVLHQDWLNGKEYKCKVSNKALPAP 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                     421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
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FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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Sequence 12, Application US/08487550
Patent No. 613898
GENERAL INFORMATION:
FATEL OF INVENTION: MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACBUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS'
NUMBER OF SECURACES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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                                                                                                                                                                                                                                  241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPTLMISKTPEVTCVVVDVSHEDP 300
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                                                    Gaps
                                                 0;
Length 476;
                                                    Indels
100.0%; Score 2577; DB 4;
100.0%; Pred. No. 4.6e-206;
ative 0; Mismatches 0;
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REPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995
                                                 0;
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699 Prince Street
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October 2, 2003, 09:18:44; Search time 178.695 Seconds (without alignments) 421.442 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                            1 MKHLWFFLLLVAAPRWVLSQ...........MHEALHNHYTQKSLSFGK 476
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/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             587654 seqs, 158212981 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2577
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:* /cgn2_6/ptodata//2/pubpaa/US10_NRW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NRW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_NBW_PUB.pep:*

6/ptodata/2/pubpaa/US10A_PUBCOMB. 6/ptodata/2/pubpaa/US10B_PUBCOMB.

/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

Description	Sequence 4, Appli Sequence 4, Appli	4.4.	Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl	12,	Sequence 8, Appli Sequence 10, Appl	4 4 (29)
SUMMARIES	US-10-1248-429B-4 US-10-124-807-4	US-IU-Z9I-33Z-4 US-10-124-905-4 US-00-040-420B-12	US-10-124-807-12 US-10-124-807-12 US-10-291-532-12	US-10-124-905-12 US-10-211-357-12	US-10-211-357-8 US-10-211-357-10 US-09-925-179-66	US-09-920-171-14 US-09-920-171-16 US-09-925-179-65
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% Query Match Length DB	476	4 4 4 0 7 4 0 7 4	476 476 476	476	467 704 704 104	451 451 451
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Score	2577	2577	2309 2309	2309	2111.5 2104.5 2103	2100 2100 2100
Result No.	100	J 4 R	John	დ თ (111	11131

Sequence 14, Appl	Ĭ		8		7	6	23	æ	ထ	ထ	_	Sequence 8, Appli		-	7	m	4	4	Š	ici	7,	23(Sequence 230, App	'n	ω	'n.		ž	Sequence 218, App
966-	2 US-10-113-996-16	1 US-09-925-179-68	US-09-920-171-18	2 US-10-113-996-18	2 US-10-292-869-2	2 US-09-792-938-2	US-09-740-002-25	0 US-09-948-429B-8	2 US-10-124-807-8	2 US-10-291-532-8	4 US-10-124-905-8	US-09-802-077-8	US-09-802-096-8	1 US-09-925-179-8	1 US-09-726-258-71	2 US-10-310-719-37	5 US-10-171-452A-41	5 US-10-171-452A-47	5 US-10-171-452A-59	5 US-10-171-452A-53	US-09-740-002-27	0 US-09-996-288-230	1 US-09-996-265-230	2 US-10-225-108A-3	\mathbf{a}	US-09-796-848A-43		0 US-09-996-288-216	-09
451 1	451 I	451 1	451 9	451 1	451 13	451 1	475 9	478 1	478 1	478 1	478 1	453 9	453 9	453 1	452 1	580 13	467 1	467 1	467	467 1	475 9	451 1	451 1	474 1	474 1	450 9	450 9	450 1	450 1
81.5	61.5	81.5	81.2	81.2	81.2	81.2	80.5	80.4	80.4	80.4	80.4	80.3	80.3	80.3	80.0	79.7	79.7	79.7	79.7	79.6	79.5	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4
2100	710	209	2093	2092	2093	2093	2075.	2073	207	2073	2073	206	2069	206	2061.	205	2053.5	2053.5	2053.	2050.	2047.	2047	2047	2046	2046	2045.	2045.5	2045.	2045.
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ALIGNMENTS

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RESULT 1

RESULT 1

Sequence 4, Application US/09948429B

TITLE OF INVENTION: MONKEY MONOCIONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: MONOCIONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: IMMUNOSUPPRESANTS*

TITLE OF INVENTION: IMMUNOSUPPRESANTS*

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSER: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 PRINCE Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: SIP 22314

COMPUTER READABLE FORM:

MUDIUM TYPE: Floppy disk

COMPUTER: IEM PC Compatible

COMPUTER: IEM PC Compatible

COMPUTER: IEM PC Compatible

COMPUTER: PALONIC NOTE: PODS/NS-DOS

SOSTWARE: PALONIC NOTE: DOS/NS-DOS

SOSTWARE: PALONIC NOTE: DOS/09/948,429B

FILING DATE: O'-CUN-1995

APPLICATION NUMBER: US 08/08/487,550

RELIGATION NUMBER: US 09/08/487,550

RECIETRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 31-012/12-131

TELEOPMONICATION INDEMBRICOR: TELEOPMONICATION NUMBER: 101-1121

TELEOPMONICATION NUMBER: 31-06-20
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PRIOR APPLICATION DATA:
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US-10-291-532-4
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
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                                                                                                                                                                                                 Gaps
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                                                                                                                                                       Query Match
100.0%; Score 2577; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.8e-179;
Matches 476; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10124807; Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4.76 amino acids
TYPE: amino acid
TOPOLOGY: linear
703-836-2021
                                                                                                     ; MOLECULE TYPE: protein US-09-948-429B-4
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 TELEFAX:
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US-10-124-807-4
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APPLICANT: HANNA, NABIL
TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: ADDIATED KILLING OF B CBLL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
CURRENT APPLICATION NUMBER: 021002-11-12
CURRENT APPLICATION NUMBER: 60/311,187
PRICA PAPLICATION DATE: 2001-11-10
PRICA FILING DATE: 2001-11-10
PRICA THING DATE: 2001-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGXYYWTWIRQT 60
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100.0%; Score 2577; DB 12; Length 476;
Best Local Similarity 100.0%; Pred. No. 4.8e-179;
Matches 476; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                             012712-131
                                                     US 08/487,550
APPLICATION NUMBER: 09/383,916
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                                                                                                                                                               35,030
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                               FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                     NAME: Teskin, Robin L. RECISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                       703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-10-124-807-4
                          FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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October 2, 2003, 13:01:50; Search time 1891.24 Seconds (without alignments) 15574.362 Million cell updates/sec
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720
1 ATGAGCCTCCCTGCTCAGCT.....TCAACAGGGGAGGTGTTGA 720
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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em_htgo_other:*

em_htgo_hum:*

htg_rod:* em_htq_mam:* em_htg_vrt:*

PAT 14-FEB-2001

linear

DNA

ALIGNMENTS

720 bp Sequence 5 from patent US 6113898. AR108864. AR108864.1 GI:12825140

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 1 AR108864 LOCUS

Unknown. Unknown.

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL

Unclassified.

1 (bases 1 to 720)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C. Human BY.1-specific primatized antibodies and transfectomas expressing said antibodies
Patent: US 6113898-A 5 05-SEP-2000;

AB064104 Homo sapi AB064054 Homo sapi E10698 cDNA encodi

Ното

AB064055 Homo s AB064058 Homo s AB064112 Homo s AB064092 Homo s AB064093 Homo s AB064093 Homo s

AR108864 Sequence
AR265198 Sequence
BD065036 Identific
BC022362 Homo sapi
E40698 Antihuman F
E40697 Antihuman F
E50697 Antihuman F
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E55207 Human monoc
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E55209 Human monoc Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Homo AB064059 FAB064137 FAB064137 FAB064101 FAB0641 AB064136 AB064135 AB064105 AB064057 SUMMARIES AX067347 AB064106 E35205 E35207 E35208 E35204 AB064102 E35201 E35206 E35203 E40598 E40748 E40696 E40697 E40695 BC030814 BC034142 AK096938 E35209 E35210 AB064059 DB Length Query Match Score 620.4 618.8 618.8 617.2 607.6 599.6 599.4 598.8 598.2 5591.6 5881.6 5881.7 5883.7 5883.7 5883.7 583.7 583.7 590.8 590.8 590.8 590.8 590.8 590.8 601.2 Result Ş

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Location/Qualifiers
                    /organism="unknown"
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Homo sapiens (human)
Homo sapiens
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Aguin,S. and Vezina Louis.-P.
Method for producing polyhydroxyalkanoates in recombinant organisms
Patent: US 6422134-A 5 10-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear PAT 10-APR-2003
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                                                                Query Match 100.0%; Score 720; DB 6; L Best Local Similarity 100.0%; Pred. No. 1.6e-194; Matches 720; Conservative 0; Mismatches 0;
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1 (bases 1 to 720)
Anderson, D.R., Hanna, N., Brams, P. and Hard, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BD063036 127-AUG-Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
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                                                                         Length 720;
                                                                      100.0%; Score 720; DB 6; Length 7 llarity 100.0%; Pred. No. 1.6e-194; Conservative 0; Mismatches 0; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

October 2, 2003, 12:12:30 ; Search time 147.469 Seconds (without alignments) 13179.730 Million cell updates/sec Run on:

US-09-758-173-5 Title:

Perfect score:

720 1 AIGAGCCTCCCIGCTCAGCT......TCAACAGGGGAGGTGTTGA 720 Sequence:

IDENTITY_NUC Gapopt 1.0 Scoring table:

2552756 seqs, 1349719017 residues Searched:

5105512 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_19Jun03;* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Macaque primatized	DNA sequence of a	Primatised anti-hu	Anti-human Fas hum	Anti-human Fas imm	Human immunoqlobul	Anti-human Fas Iq	Anti-human Fas hum
スコイン			:			_	^1	_	~	_	_
SUMMARIES		di		AAV35486	AAS17244	AAT62511	AAV61362	AAA7827(AAV66632	AAA78320	AAV61360
		DB	1	19	24	18	19	21	19	21	19
		Query Match Length DB		720	720	720	720	720	891	891	720
	dР			100.0	100.0	99.8	86.4	86.4	86.2	86.2	85.9
		Score		720	720	718.4	622	622	620.4	620.4	618.8
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ALIGNMENTS

AAV35486 standard; DNA; 720 BP. RESULT 1 AAV35486

29-SEP-1998 (first entry) AAV35486;

Macaque primatized 7B6 light chain DNA.

Monoclonal antibody, Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; . T cell/P cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IGG; immunoglobulin G; T cell proliferation; ss.

Macaca fascicularis.

/*tag= a /product= 7B6 light chain Location/Qualifiers 1..720 /*tag= a

WO9819706-A1

14-MAY-1998.

97WO-US19906. 29-OCT-1997;

96US-0746361. 08-NOV-1996;

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This sequence encodes a primatized form of the antibody 7B6 light chain macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host disease, B cell lymphoma, infections (including by human immune to be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin.2 (IL-2), T cell proliferation and multiple responses.
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                                                                                                                                                New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting bloding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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                                          Hanna N;
(IDEC-) IDEC PHARM CORP
                                          Brams P,
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P-PSDB; AAW63762.
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481 CIGAATAACTICTAICCCAGAGAGAGCCAAAGIACAGIGGAAGGIGGAIAACGCCCICCCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective, apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80, B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autolmmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of a primatised form of the light chain of 7B6 antibody.
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                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002 (first entry)
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Chimeric - Macaca sp.
Synthetic.
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603043095F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183446 5',
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NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Producment: Life Technologies, Inc.
cDN Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMI1457 row: n column: 23*
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Homo sapiens
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AUTHORS
TITLE
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COMMENT
   BI759427 603043095
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AW404795 UI-HF-BLO BU146853 AGENCOURT BX437517 BX437517

ALIGNMENTS

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/note=_Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming, Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library.
                                                                                                                                BM007808 774 bp mRNA linear EST 30-OCT-2001 603617276F1 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:5440962 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TATCAGCAGAGACAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACGGGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 GATGIIGIGAIGACICAGICICCACICTCCCIGCCGICACCCIIGGACAGCCGGCCICC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGCAGGGGACAGATTTCACACAGGAAATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 774)
Nat-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
        670 CTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGGGCTTCAACAGGGGAGAGTGTT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contract: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1914 row: h column: 19
High quality sequence stop: 770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 610.6; DB 12; Length 774; Pred, No. 1.7e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5440962"
/tab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                     BM007808.1 GI:16522162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%;
91.6%;
                                                                                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.6<sup>5</sup>
Matches 657; Conservative
                                                                                                                                                                                     mRNA sequence.
BM007808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
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                                                                                                                                LOCUS
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ORIGIN
                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                 RESULT 2
BM007808
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                                                                                            /MOL_type="mRNA"
//MOL_type="mRNA"
//do_xref="taxon:9606"
//clone="inAgne:518346"
//lab_host="inAgne:518346"
//lab_host="inAgne:518346"
//lab_host="inAgne:518346"
//lab_host="inAgne:518346"
//lab_host="inAgne:518346"
//note="Organ: pooled colon, kidney, stomach; Vector: pcMv-SPORN6; Site_1: Noti: Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is classificated for full-length clones and was constructed by C gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAAGTIGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGCAGGGACAGATTTCACACTGAAAATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TCTGACGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CCCACTITCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 CGGACGTTCGGCCAAGGGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATCTGTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGGTCCAGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618.8; DB 12; Length 816;
Pred. No. 8.8e-163;
0; Mismatches 62; Indels 0;
                                                                           /organism="Homo sapiens"
ity sequence stop: 814.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.9%;
ilarity 91.4%;
Conservative (
High quality
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656; Conserv
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Best Local 9
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ORIGIN
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IS POPOLALIA
COMPUTER: IS PROPERATIONE
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-101-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 703-836-6620
TELEFRAX: 703-836-6620
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US-09-335-697B-16
US-09-335-697B-16
US-08-376-852-152
US-08-276-852-152
US-08-899-575-152
US-08-899-575-168
US-08-899-575-168
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US-08-899-575-168
US-08-899-575-168
US-08-276-852-170
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US-08-276-852-170
US-08-899-575-156
US-08-899-575-156
US-08-899-575-156
US-08-899-575-175
US-08-899-575-175
US-08-899-575-175
US-08-899-575-175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 720;
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                           US-08-487-550-5; Sequence 5, Application US/08487550; Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 base pairs
nucleic acid
EDNESS: not relevant
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F: 699 Prince Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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   1..720
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STREET: 69
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FEATURE:
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US-08-487-550-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
STATE:
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APPII
APPII
APPII
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                                                                                                      2, 2003, 13:10:05; Search time 38.2657 Seconds (without alignments) 8304.972 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5, Al
Sequence 55,
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Sequence 55,
Sequence 55,
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1 ATGAGCCTCCCTGCTCAGCT......TCAACAGGGGAGAGTGTTGA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*

'Gqn2_G/ptodata/2/ina/5A_COMB.seq:*
'Gqn2_G/ptodata/2/ina/5B_COMB.seq:*
'Gqn2_G/ptodata/2/ina/6A_COMB.seq:*
'Gqn2_G/ptodata/2/ina/BE_COMB.seq:*
'Gqn2_G/ptodata/2/ina/PCTUS_COMB.seq:*
'Cqn2_G/ptodata/2/ina/PCTUS_COMB.seq:*
'Cqn2_G/ptodata/2/ina/PCTUS_COMB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-491.334A-55
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US-08-488-376-16
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
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TOPOLOGY: linear MOLECULE TYPE: peptide
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US-09-526-098-5
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMB B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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                                             1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCGGGTCCAGTGGG
                                                             1 ATGAGCCICCCTGCICCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG
                                                                                                   121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG
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                  0; Indels
 Pred. No. 4e-203;
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Patent No. 6492134
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
100.0%;
                 720; Conservative
   Best Local Similarity
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                   SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                              012712-131
                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 720; Conservative
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/ cgn2_6/ptodate/2/pubpna/PGT_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB :
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Sequence 105, App Sequence 33, Appl Sequence 14, Appl Sequence 41, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 49, Appl Sequence 5, Appl Sequence 5, Appl Sequence 6, Appl Sequence 10, Appl Sequence 51, Appl	
2-6556-11 2-6556-11 2-6556-11 2-6556-11 2-6556-11 2-6556-11 2-6556-11 2-6556-11 2-656-11	J-158-646 9-822-830
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ALIGNMENTS

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Sequence 5. Application US/09948429B
Sequence 5. Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Frince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 22314
COUNTRY: USA

CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
APPLICATION NUMBER: US 08/487,550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFRAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                        STREET: 699 Princ
CITY: Alexandria
STATE: VA
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US-09-972-656-103

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TITLE OF INVENTION: "MONREY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GAAGITGIGAIGACTCAGICTCCACTGICCCTICCCATCACACCTGGAGAGCCGGCCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
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                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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RR: 012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Testin, Robin L.
REGISTARITON NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-13
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
     Anderson, Darrell R.
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TELEPHONE: 703-836-6620
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MEDIUM TYPE: Floppy
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, LOCATION:
US-10-124-807-5
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LOCATION:
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   APPLICANT:
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                                                                                                                                                                                                                                                                       tch 100.0%; Score 720; DB 10; al Similarity 100.0%; Pred. No. 2.2e-221; 720; Conservative 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                NAME/KEY: mat_peptide LOCATION: 1..720
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                     linear
                                                                                                                                                           1..720
                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                             LOCATION:
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US-09-948-429B-5
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Matches 73
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Primatised anti-hu Macaque primatized Protein sequence o Anti-human Fas hum Anti-human Fas hum Anti-human Fas hum Anti-human Fas hum Anti-human Fas hum Anti-human Fas hum
SUMMARIES	AAW01819 AAW03762 AAW11540 AAW71879 AAW12916 AAW71877 AAW71878 AAW71878 AAW12914
DB	221222222222222222222222222222222222222
% Query e Match Length DB	
% Query Match	0.0001
Score	1242 1242 1242 1116 1113 1113 1113
Result No.	

Anti-human Fas hum Anti-human Fas imm	PTHrP mon	MDDT	•—	Calx		Human PTHrP monocl	Human PTHrP monocl	Human PTHrP monocl	Human PTHrP monocl	3F4 Human IgG4 exp	Murine anti-porcin	Human PTHrP monocl	mon	13	Humanised 3D6 anti	p	\neg	sed	in #1 i	PTHrP	PTHrP mo	chain. H	ised anti-	sed 266 a	sed 323/	sed 323/A	sed 323/A	sed 323/	ised 3D6 an	recombinan	Mucin 1 (MUC-1) bi	tor pMDR100	lanis	Humanised anti-Fas
AAW71876	261	7033	5828	1845	3261	3261	3261	3261	3261	194	ω	197	197	530	327	74	55	ABP58286	28	걾	261	0	946	331	N	223	223	223	327	271	380	380	3303	77
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ALIGNMENTS

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Monoclonal antibody; cynomolgus monkey; macaque; 7B6; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                             Primatised anti-human B7.1 antigen antibody 7B6 light chain.
                                                                                                                                                                                                                                                                                                                                                                   Shestowsky WS;
                      AAW01819 standard; Protein; 239 AA
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                                                                                                                                                                                                                                                                                          96WO-US10053.
                                                                                                                                                                                                                                                                                                                 95US-0487550.
                                                                                                                                                                                                        Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Anderson DR,
                                                                                                                                                                                                                                           WO9640878-A1.
                                                                      25-MAY-1997
                                                                                                                                                                                                                                                                                          06-JUN-1996;
                                                                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                    19-DEC-1996
                                              AAW01819;
RESULT 1
AAW01819
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                          61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                              PIFGGGTKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody, Mab, macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Tell/R cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idlotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGNSOESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 786. Cloned 786 light and heavy variable genes (see also AAT62811 and AAT13847) are inserted into an expression vector (pref. NBOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01817-19 and AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                            1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                           1 MSLPAQLIGILICVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDIFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                  Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                        100.0%; Score 1242; DB 18; Length 239; 100.0%; Pred. No. 1.8e-69; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaque primatized 7B6 light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW63762 standard; Protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brams P, Hanna N;
                                                                        Claim 8; Fig 9A; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0746361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                    239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca fascicularis.
WPI; 1997-108638/10.
                                                                                                                                                                                                                                                  239 AA;
                                                                                                                                                                                                                                                                                         Similarity
            N-PSDB; AAT62511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9819706-A1.
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                                                                                                                                                                                                                                                    Sednence
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                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                  Matches
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This sequence represents a primatized form of the antibody 7B6 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigons and inhibits binding of these antigons to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving really earli interactions, particularly autoimmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression, and interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQQKPGQPPALLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVBAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, macaque monkey; light chain; primatised antibody; 786 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86, B cell cancer; metastasis; tumour; B cell lymphoma; B cell letkaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLPAQLLGLILLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                    New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD2B - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1242; DB 19
100.0%; Pred. No. 1.8e-69;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-2; IL-2; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU11540 standard; Protein; 239 AA
                                                                                                                                                                                                                                                Example 7; Fig 4a; 87pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
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Chimeric · Macaca sp.
1998-286601/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AA;
                       N-PSDB; AAV35486
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 2, 2003, 09:07:34 ; Search time 10.503 Seconds Run on:

(without alignments) 2188.349 Million cell updates/sec

US-09-758-173-6

1242 1 MSLPAQLLGLLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239 Perfect score: Sequence:

BLOSUM62 Scoring table:

283308 seqs, 96168682 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

pir1:*
pir2:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	script	kappa chain	kappa chain	kappa chain	kappa chain	~	kappa chain	~	kappa chain V	×	×	×	kappa chain pr	~	kappa chain -	kappa chain V	kappa chain (M	noclonal anti	kappa chain	kappa cha	kappa chain pr	kappa chain	kappa cha	kappa chain -	kappa chain V-	-kappa	kappa chain pr	kappa chain pr	chain pr	NVK protein pre
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RESULT 2

ig Kappa chain NIG26 precursor - human (Specias: Homos Sapiens (Man) (C) Specias: Homos Sapiens (Man) (C) Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 (C) Accession: JE0242 (R) Accession: JE0242 (R) Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIFID, November 1998 (A) Description: Structure relationship of Kappatype light chains with AL amyloidosis:

A;Molecule type; protein A;Residues: 1-215 GALT-C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology <IMM>

A; Reference number: JE0241 A; Accession: JE0242

Ig kappa chain V-J	19 happa chain VI	Ig kappa chain C r	19 kappa chain V r Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain V r	Ig kappa chain - h	Ig lambda-like cha	Ig kappa chain - h	Ig kappa chain - h	Ig kappa chain - h	Ig kappa chain C r	Ig kappa chain pre	anti-digoxin trans
\$40357	S40324	КЗНО	S22902 S40342	A24452	S26882	S40373	A49633	S40312	540322	S40355	A37927	PL0106	PH0106
77	1 7		N (1	Н	7	7	N	Ġ	7	N	7	~	C)
136	133	106	135	133	132	128	238	126	132	131	66	144	132
44.4	44.2	44.1	44.1 43.6	43.3	43.2	43.0	42.9	42.2	41.9	41.8	41.3	41.1	40.9
552	549	548	541	538	537	534	533	524	520	519.5	513	510.5	508.5
30	35	33	ω ευ 4. ευ	36	37	80 E	36	40	41	42	43	44	45

ALIGNMENTS

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Ig kappa chain NIG2 precursor - human C;Species: Homo Sapiens (man) C;Species: Homo Sapiens (man) C;Species: Homo Sapiens (man) C;Accession-10004 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C;Accession: JE0244 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 S;Accession: JE0244 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 #text_change 21-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPP-TFGGGTKVEIKRTVAAPS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 VFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 915; DB 2; Length 215; pred, No. 2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-215 <ALI-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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80,9%; Pred. No. ze.
"ve 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73;7%
Best Local Similarity 80,9%
Matches 178; Conservative
RESULT 1
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin P;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                Query Match 69.2%; Score 860; DB 2; Best Local Similarity 78.4%; Pred. No. 1.1e-51; Matches 171; Conservative 18; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-216 <ALI>
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C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
B;Leoni, J; Ghiso, J; Goni, F; Frangione, B.
J; Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogla A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Acces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL A; Reference number: JE0243
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                                                                                                                                                                                        21 EVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
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                                                                                                                        4; Gaps
                                        y Match 73.1%; Score 908; DB 2; Length 215; Local Similarity 79.9%; Pred. No. 5.9e-55; hes 175; Conservative 19; Mismatches 21; Indels
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A;Residues: 1-215 <ALI7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A submitted to the EMBL Data Library, August 1994
A; Description: Coordinate expression of antibody subunit genes yields high levels of A; Reference number: $52028
A; Accession: $52028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig Rappa chain Am37 precursor - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 (Spacession: JED2A) (November 1998 (Spalim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JPPD, November 1998 (Species of Apparagoration: Structure relationship of Kappatype light chains with AL amyloidosis: A; Reference number: JED241
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C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: $52028
                                                                  4; Gaps
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Length 215;
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                                                                  25; Indels
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us-09-758-173-6.rsp

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OM protein - protein search, using sw model

October 2, 2003, 08:56:23 ; Search time 6.59233 Seconds (without alignments) 1704.917 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-758-173-5 1242 1 MSIPAQLIGILLICVPGSSG......EVTHQGLSSPVTKSFNRGEC 239

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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1D5B; 09-FEB-00.
1D5I; 09-FEB-00.
1D6V; 04-OCT-00.
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57
106 AA;
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Best Local Similarity
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                                                            61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
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                                 1 MRLPAQLIGILMIWVPGSSGDVVWTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW
                     1 MSLPAQLIGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                      SEQUENCE (MYELOMA PROTEIN EU).
MEDLINE-71064023; PubMed-5489770;
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Gaps
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and J region
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Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
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(In Franch F., Shugar D. (eds.);
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                       KAC_HUMAN STANDARD; PRT; 106 AA. P01834; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 1GKC.
 Mismatches
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MEDLINE=68242259; PubMed=5586923;
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MEDLINE=71064027; Pubmed=4923144;
 13;
                                                                                                                     121 WTFGQGTKVEIKR 133
                                                                                                        121 PIFGGGTKVEIKR 133
  Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its ong its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3550(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
MEDLINE-70201507; PubMed-5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FTIG-VAR_003097.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).
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Pred. No. 2e-37;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: 00:0003823; F:antigen binding activity; NAS. GO; GO:0008955; P:immune response; NAS. InterPro; IPR007110; Ig-11ke. InterPro; IPR003597; Ig_c1. InterPro; IPR003597; Ig_c1. InterPro; IPR003006; Ig_MHC. Pfam: PF00047; Ig; 1. Rol: InterPro; IRCI; 1. Rol: IRCI; IRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 2e-
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-33; 38-41 AND 62-80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Abdominal adipose tissue; PubMed=9588180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00241; AAA58989.1; -. EMBL; V00557; CAA23823.1; -.
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PDB; 1HKL; 12-MAG-01.
PDB; 1172; 08-AUG-01.
PDB; 1MIM; 15-MAY-97.
Genew; HGNC:5716; IGKC.
MIM; 147200; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 169:56-59(1970).
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Searched:

Database

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61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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280.355 homo s 980.811 homo s 288.414 homo s 288.414 homo s 291.82 mus n 295.616 homo s 299.117 homo s 291.85 homo s 291.85 homo s 291.85 homo s 291.87 homo s 291.87 homo s 291.77 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; BCO23362; AAH2362.];
InterPro; IPR003106; Ig_MHC.
R InterPro; IPR003306; Ig_MC.
R InterPro; IPR003596; Ig_W.
R Pfam; PF00047; Ig; 2.
R PARRT; SM00406; IGv; 1.
R PROSTIE; PS50299; IG_MHC; 1.
R PROSTIE; PS00299; IG_MHC; 1.
Hypothetical protein.
W Hypothetical protein.
O SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AA
                                                            QBWUKA
QBVIR2
QBVII22
QBSMII22
QBSMII22
QBVII78
QBVII78
QBUIR36
QBUIR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-NAR-2003 (TrEMBLrel. 23, Hypothetical protein. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                      [1]
SEQUENCE FROM N.A.
TISSUE=Lung;
      Q8TCD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
    QBTCD0
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                                                                                                                                   2, 2003, 08:56:23; Search time 23.129 Seconds (without alignments) 2666.544 Million cell updates/sec
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                                                                                                                                                                                                              US-09-758-173-6
1242
1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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Q8nek0 homo s
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                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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Q8KQF8
Q8KQF0
Q91WF8
Q91W12
Q91WS9
Q91WS9
Q9RLA5
Q9RLA5
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Q99M37
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Q8NEK0
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Gapop 10.0 , Gapext 0.5
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5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_bacteriap:*
sp_archeap:*
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9: sp_phage:*
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2: sp_bacteria:*
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Match Length DB
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Maximum DB
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Gaps

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Result Š.

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PRT;
                                          Strausberg*, strausberg*, submitted (JUN-2002) to the EMBL BMBL; BC030813; AAH30813.1; InterPro: IPR00110; Ig-11ke. InterPro: IPR003597; Ig_c1. InterPro: IPR003597; Ig_c1. InterPro: IPR003506; Ig_MHC. InterPro: IPR003596; Ig_WHC. InterPro: IPR003596; Ig_W. SMART; SM00407; Igc1; IsMART; SM00406; IgV; I. SMART; SM00406; IgV; I. PROSITE; PS050835; IG_IKE; 2. PROSITE; PS0299; IG_MHC; I. Hypotheiical protein. SEQUENCE 234 AA; 25530 MW; 6
                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8 Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
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                              TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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Q8VCI6;
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                            PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                          SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSLPAQILGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                 Q8NEKO;
Q8NEKO;
Q1-0CT-2002 (TTENBLrel. 22, Created)
Q1-0CT-2002 (TTENBLrel. 23, Last sequence update)
Q1-0CT-2003 (TTENBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia: Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITARY OF TEMBLIE 1. 22, Created)
01-OCT-2002 (TIEMBLIE 1. 22, Last sequence update)
01-MAR-2003 (TIEMBLIE 1. 23, Last annotation update)
Hypothetical protein.
Hymorhetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC030814; ARH30814.1; -.
InterPro: IPR007110; Ig-11ke.
InterPro: IPR0073597; Ig_c1.
InterPro: IPR003596; Ig_WHC.
InterPro: IPR003596; Ig_W.
Pfam; PF00047; Ig; 2.
SMART; SM00407; IGc1; 1.
SWART; SM00406; IGY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;
                                                                                                                                                                                        239 AA
                                                                                                                                                                                        PRT;
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                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
             121
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                                                                                                                                                       RESULT 2
Q8NEK0
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QBNEK1
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61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                     76.4%; Score 949.5; DB 4; Length 234; 77.8%; Pred. No. 4.3e-79; ive 24; Mismatches 24; Indels 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1; ..
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_Lv.
SMART: SR004045; Igy. 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              6316E8DEF8D132F8 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kba protein.
Mus musculus (Mouse).
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Appl Appli Appli

Sequence Sequence S

Sequence Seq

Sequence Sequence Sequence Sequence

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ADDRIGONT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: PHARMACEUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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ZUP: 22314
COMPOTER: ELOPDY disk
COMPUTER: IBM PC COMPACAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
ATTON NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
ATTONEV/AGENT INFORMATION:
REGISTRATION NUMBER: 35,030
RESPERENCE/DOCKET UNBER: 35,030
RESPERENCE/DOCKET UNBER: 35,030
REJEPRA: 703-836-6620
TELEPRA: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1242; DB 3; Best Local Similarity 100.0%; Pred. No. 3.9e-101; Matches 239; Conservative 0; Mismatches 0;
US-09-027-449-56
US-08-804-444A-56
US-09-026-56
US-09-234-340A-56
US-09-301-593-28
US-08-952-235-1
US-08-952-235-1
US-09-740-002-24
US-08-895-71-1
US-08-895-75-153
US-08-899-575-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08487550 Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : LENGTH: 239 amino acids:
TYPE: amino acid
TOPELOGY: linear
NOLECULE TYPE: protein
     GENERAL INFORMATION:
     RESULT 1
US-08-487-550-6
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                                                                                                                                                                                                                                                                                 US-09-758-173-6
1242
1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-398-613A-56
US-08-398-612A-56
US-08-998-612A-56
US-09-027-449-42
US-09-027-449-42
US-09-026-985-42
US-09-301-593-36
US-09-301-593-36
US-09-026-985-62
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US-09-026-985-51
US-09-121-952A-51
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB
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                                                                                                                                                                                    Run on:
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Length 239; Indels

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APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
ITLE OF INVENTION: ANTI-CO4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 179
SGNSQESVIEQDSKDSTYSLSSTLILSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                          181 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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4.7e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION: WORD STATES
APPLICATION: 424
CLASSIFICATION: 424
APPLICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
COMPRESS: COORDINGS
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                                                                                                                                                                                                                                                                                                                                            Sequence 56, Application US/07916098A Patent No. 5871732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 92,3
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 715-1234
TELER: 910/221-5314
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26,949
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NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETT
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-916-098A-56
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                                                                                                                                                                                                                                                                                           RESULT 3
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Patent No. 6492134

GENERAL INFORMATION:

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNG, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                      61. YQQXPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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           YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
Classification Application Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239; Conservative
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; Search time 89.7228 Seconds (without alignments) 421.442 Million cell updates/sec
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1242
1 MSLPAQLIGILLLCVPGSSG.....EVTHQGLSSPVTKSFNRGEC
    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                   hits satisfying chosen parameters:
                                                                                         587654 seqs, 158212981 residues
                                                                                                                                               Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                         protein search, using sw model
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US-10-171-452A-44 US-09-922-698A-24 US-09-972-656-94 US-09-972-656-94 US-10-384-933-107 US-10-216-484-107 US-10-216-484-109 US-10-216-484-109 US-10-216-484-109 US-10-216-484-109 US-10-216-484-109 US-10-216-484-52 US-10-384-933-52 US-10-384-933-52 US-10-384-933-50 US-10-10-384-933-50 US-10-10-388-15 US-10-10-10-388-15 US-10-10-10-388-15 US-10-10-10-38-15 US-10-98-88-88-4

ALIGNMENTS

Appl Appl

Sequence 4 Sequence 5 Sequence 1

US-10-171-452A-45 US-10-171-452A-51 US-10-384-933-129

Sequence 8,

Sequence

Sequence 3 Sequence 5 Sequence 1

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US-05-948-429B-6

US-05-948-429B-6

Sequence 6, Application US/09948429B

Patent No. US2002017689A1

GENERAL INFORMATION:

MONETE OF INVENTION: "WONEY MONCCIONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: "WONEY NO. TO HUMBAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: TO HUMBAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS TITLE OF INVENTION: IMMUNSUPPRESANTS'

TITLE OF INVENTION: TO HUMBAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS UNMER OF SEQUENCES: 12

CONFESPONDERS OF SEQUENCES: 12

CONFUTE: 099 Frince Street

CITY: Alexandria

STATE: WAS ADDITED TO COMPUTE: TEM PC COMPUTES: TEM PC COMPUTES: TE DEPOSITION STREET: CP-DOS/MS-DOS

COMPUTES: PEACHLIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PRICA SPELICATION DATA:

APPLICATION NUMBER: US/09/948,429B

FILING DATE: DATE OF TOWNINGER: US/09/948,7550

ATTORNEY ARGAIN NUMBER: US/09/948,7550

ATTORNEY AGENT INFORMATION:

REGISTRATION NUMBER: 35,030

ATTORNEY AGENT INFORMATION:

NAME: TEACHON NUMBER: 35,030

TELEDPOONE: 703-836-6620
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Match

Score

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Query

Result

1: / cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: / cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
3: / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: / cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: / cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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14: / cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
15: / cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
16: / cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
17: / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
11: / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
11: / cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-09-948-429B-6 US-10-114-807-6 US-10-291-532-6 US-10-124-905-6 US-09-922-600A-8 US-09-924-340-8 US-09-929-570-8 US-10-154-678-8 US-10-100-489-8 US-10-000-489-8 US-10-000-489-8 US-10-000-986-8 US-10-111-452A-38 US-10-111-452A-38 US-10-111-452A-38

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1242 12442 10242 1068 1068 1068 1068 1068 1003 1003 997

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Sequence 6,

Description

Sequence Seq

Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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ORGANISM: Artificial Sequence
                                                                                                           Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-6
                                                                         Query Match
Best Local Similarity
Matches 239; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-291-532-6
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                       PIFGGGIKVEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                           1 MSLPAQLIGILILICVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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                                                                                                                                                                DB 10;
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                                                                                                                                                 100.0%; Score 1242; DB 10; 100.0%; Pred. No. 7.2e-78; Wiematches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                Best Local Similarity 100.
Matches 239; Conservative
                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 239 amino acids TYPE: amino acid
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     703-836-2021
                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-4298-6
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MEDIUM TYPE: Floppy
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Publication No. US20030180290A1
GENERAL INFORMATION:
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, MABIL
TITLE OF INVENTION: AMEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR INTELS PRESENCE: 037003/291872
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REPEREBRENCE: 037003/291872
CURRENT APPLICATION NUMBER: 60/331,187
PRIOR PLICATION NUMBER: 60/331,187
PRIOR PLING DATE: 2001-11-09
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PLING DATE: 2001-01-12
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                  1 MSLPAQLIGILLICVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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100.0%; Score 1242; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 239; Conservative 0; Mismatches 0;
Score 1242; DB 12;
Pred. No. 7.2e-78;
Mismatches 0;
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0
     100.0%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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October 2, 2003, 13:01:50 ; Search time 3774.61 Seconds (without alignments) 15574.362 Million cell updates/sec US-09-758-173-7 1437 1 ATGGGITGGAGCCICATCII......CCCIGICICCGGGIAAAIGA 1437 5777422 Total number of hits satisfying chosen parameters: 2888711 seqs, 20454813386 residues OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

GenEmbl:*

gb_ow:*
gb_pat:*
gb_ph:*
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gb_rs:* em_sts:* em_un:* em_fun: em_om:* em_or:* gb_ba:* gb_htg:* gb_in:* em_hum: em_pat: em_mu: em_in: Database :

Pred. No. is the number of results predicted by chance to have a

em_htgo_other:* em_htgo_hum: * em_htgo_mus: *

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR108865 Sequence AR265199 Sequence BD063037 Identific AK093806 Homo sapi AX080951 Sequence	BC014667 Homo sapi BC006402 Homo sapi BC018747 Homo sapi BC024289 Homo sapi AY172959 Homo sapi AX11855 Sequence A21385 Plasmid DNA Y14737 Homo sapien AK097859 Homo sapien	AK098817 Homo sapi AK098817 Homo sapi BD075127 Method fo AK097010 Homo sapi BC019046 Homo sapi Y14735 Homo sapi AK097367 Homo sapi AF015036 Synthetic AF015036 Synthetic AF015036 Homo sapi AK097350 Homo sapi	AK097206 Homo sap1 AX594307 Sequence AX616608 Sequence AX616610 Sequence AX010615 Sequence AX010645 Sequence AX010645 Sequence AX0172957 Homo sap1 AX097366 Homo sap1 AX277242 Sequence AX330501 Sequence AX330501 Sequence AX3330501 Sequence AX33307 Sequence AX333107 Sequence AX333107 Sequence AX333107 Sequence AX333107 Sequence	A2585 Human (1721, A2586 Human CA2586 Human CA25840 Antigen-b BD078408 Antigen-b AX556949 Sequence	DNA linear PAT 14-FEB-2001 Shestowsky,W.S. and Heard,C. bodies and transfectomas
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% Quer ore Matc	4437 100.0 88.6 88.2 84.8	208 82.7 5.2 82.5 5.2 82.5 185 82.5 1.8 82.5 1.6 82.4 82.4 82.4	1103 1103 1103 1107 1107 1107 1109 1109 1109 1109 1109	1147.8 79.99 11147.8 79.99 11147.2 79.99 11147.2 79.99 11147.2 79.99 11148.1 79.94 111148.1 79.4 111138.6 79.2 11133.4 788.9 1133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 1133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 11133.4 788.9 1133.4 788.9	20.02 20.02 20.02 27.44 78.6 78.6 78.6 78.6	AR108865 Sequence 7 f AR108865.1 CURNOWN. UNCOWN. UNCOWN. UNCOWN. UNCOWNSIFIED 1 (bases 1 Anderson.D.R Human B7.1-s expressing s Patent: US 6
Result No.			11111111111111111111111111111111111111		O	AT10885 LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

QY 961 AAGCCGCGGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCTG 1020 PS 1 1 1 1 1 1 1 1 1 1	1081 GCCCCCGAGAAAACCATCCCAAAGCCAAAGGCCAGCCGGAGAACCACGGGGGTGTAC	DD	Db 1261		DEFINITION Sequence 7 from patent US 6492134. ACCESSION AR265199 VERSION AR265199.1 GI:29693620 KEYWORDS SOURCE Unknown. ORGANISM Unknown.	REFERENCE 1 (bases 1 to 1437) AUTHORS Aquin, S. and Vezina, Louis, -P. TITLE Method for producing polyhydroxyalkanoates in recombinant organisms JOURNAL Patent: US 649134-A 7 10-DEC-2002; FEATURES 1 Location/Qualifiers Source 1.1437 PARE COUNT 30 A 1610	ORIGIN OUETY Match Dest Local Similarity 100.0%; Pred. No. 1.3e-280; Matches 1437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 ATGGGTTGGAGCCTCATCTTGCTTGTGGCTGTTGCTAGGCGTGTCCAGTGTGAG 60	1	Oy 181 GGGAAGGGCCGGAATGGTAGGTTTCATTAGAAACAAACGGACGG
TURES Location/Oualifiers source 1. 1437 CCUNT 329 451 387 9. 270 GIN 100.0%; Score 1437; est Local Similarity 100.0%; Pred. No. 1	437; Conservative 0; Mismatches 0; Indels 0; 1 AIGGGIUGGAGCCTCAICTTGCTCTTGTCGCGTTTGCTACGCGTGTTCCAGT	TCTCC 12 CTCCA 18 CTCCA 18 CTCCA 18	181 GGGAGGGCCGGAATGGGTAGGTTCATTACAAACAAACGGAACGGTGGGACAACAGAA 24 241 TACGCCGCTCTGTGAAAGAATTCACCATCTCCAGAGAGTGATCCAAAAGCGAACGCTCCCAGAAGCATCGCC 30 241 TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCCAAAAGCATCGCC 30 301 MATACCAAAAGAAAGAAATTCACCAGAGATGATTCCAAAAGATCACAGAGATCACAGAGATCACAGAGATCACAGAGATCACAGAGATCACAGAGATCACAAAAGATCACAAAAGAAGAAAGA	VY 301 TAICTGAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	QY 421 GGCGCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCTTCCCCCTGGCA 480 DD 421 GGCGCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCTGGCA 480 OY 481 CCTCCTCCAAGAGCACTCTCTGGGGGCCAAGGGCCTTGGGCTCTCAGGACTAC 540	DD 481 CCTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTTTTTTT	ctacagrectcagactetacrecetrageagegi ggcacegagacetacatetgeaacgreaatgacaa 	Qy 721 AAGGIGGACAAGAAGCCCAAATCTIGIGACAAAACTCACACAIGCCCACCGIGC 780		Qy 901 GACCCIGAGGICAAGIICAACIGGIACGIGGACGGCGIGGAGGIGCAIAAIGCCAAGACA 960

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October 2, 2003, 12:12:30 ; Search time 294.323 Seconds (without alignments) 13179.730 Million cell updates/sec
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1437
1 ATGGGTTGGAGCCTCATCTT......CCCTGTCTCCGGGTAAATGA 1437
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Perfect score:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989 /SIDS1/gcgdata/geneseg/genesegn-embl/NA1990 /SIDS1/gcgdata/genesegn-embl/NA1991. /SIDS1/gcgdata/genesegn-embl/NA1992. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994 /SIDS1/gcgdata/geneseg/genesegn embl/NA1985. /SIDS1/gcgdata/geneseg/genesegn embl/NA1986. /SIDS1/gcgdata/geneseg/genesegn embl/NA1987. /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980. /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988. /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982 /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983 N_Geneseq_19Jun03;* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Macaque primatized	DNA sequence of a	Primatised anti-hu	Bicistronic chimer	cDNA sequence #572	Anti-HIV-1 recombi	Human colon cancer	cDNA of the heavy
SUMMARIES	AAV35487	AAS17245	AAT13847	AAF30315	AAS62785	AAQ49834	AAC98220	AAK98701
DB	19	24	18	22	24	14	21	54
% Query Match Length DB	1437	1437	1437	7521	1616	1386	1798	1430
	100.0	100.0	66.66	84.8	84.6	83.5	82.5	82.5
Score	1437	1437	1435.4	1219	1216	1199.2	1186	1185
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Human monoclonal r Human cDNA encodin Encodes heavy chai Traget plasmid Man Humanised 3D6 anti Plasmid Hul9GHcpcd Plasmid Hul9Hcpcd Plasmid Glambda-1B Plasmid Glambda-1B Plasmid Glambda-1B Plasmid Glambda-1B Plasmid Glambda-1B Plasmid Glambda-1B Plasmid Hul9Hcpcd Plasmid Hul9Hcpcd Plasmid Hul9Hcpcd Plasmid Hul9Hcpcd Fluman anti-HBs hea ChiTG4.12 H3 heavy Synthetic EST-deri BlWAA/P antibody h HTWAA. antibody h	Human ised anti-CD2 Human cDNA sequence #303 Human recombinant Muchi 1 (MUC-1) bi Sequence of the ch CDNA encoding a ra Human cDNA encodin Human cDNA encodin Human cDNA encodin Human cDNA encodin Lung cancer relate Antibody D heavy c Monoclonal antibod Baculovitus expres Reshaped CAMPATH-1 Plasmid pTRABac/9F	S chain; primate; antigen; CD80	autoimmune disease; IL n; imaging agent; vacci i igG; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipens and inhibits binding of these antiqens to CD28. Such MAD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumnours. Optionally the MAD as the conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, and antigen-specific immunosuppression and antigen-specific immunosuppression.
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                                                                                                                                                                                            New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1437; DB 19; Length 1437; 100.0%; Pred. No. 1.1e-277; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1437 BP; 329 A; 451 C; 387 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                               7; Fig 4b; 87pp; English
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                                                            Hanna
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Matches 1437; Conserv
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  CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC
                                          541 ITCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
                                                              TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC
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BG755166 (BQ708857 / BX415920 | BX338493 | BM007892 (BX457369)

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AGENCOURT

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1 (bases 1 to 1201)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cada - France
BMB 19
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BX414495 BX414495
BQ062878 AGENCOURT
BX337477 BX337477
                                                                                                                                                                                                                                                                           2003, 13:05:20 ; Search time 2376.47 Seconds (without alignments) 14696.420 Million cell updates/sec
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1 AIGGGTTGGAGCCTCATCTT.......CCCTGTCTCCGGGTAAATGA 1437
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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/db_xref="taxon.9606"
/clone="cSCGAP0011113"
/tissue_type="#THYMUS"
/clone_lib="Homo saplens THYMUS"
/clone_lib="Ho
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            286 GCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCKTGCTGGACTCCGACGGCT
                                                                                    GCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
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BP 191 91006 EVRY cedex - France
BP 191 9100 EVRY cedex - Grant - Fresh - WWW. genoscope.cns. fr
Gg1-bin/cluster.cg1/seq=CSOCAP001AE07NP1&cluster=7198.r. Conta
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001AE07NP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1142)
Liw.B., Gruber,C., Jessee,J. and Polayes,D.
Full.length cDNA libraries and normalization
Unpublished
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Pred. No. 3.6e-205;
6; Mismatches 9;
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Local Similarity 98.2%;
les 952; Conservative (
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                                                             /organism="Homo sapiens"
/mol_type="mkna"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized."
88 a 296 c 396 g 267 t 54 others
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